

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:29:56 ; Search time 230 Seconds
(without alignments)
1128.845 Million cell updates/sec

Title: US-10-768-886-2
Perfect score: 1953
Sequence: 1 MDGAPVAEFPRTWTHGGRYL.....DQMKQLIFNEAEMPNIY 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942.5	99.5	369	2	Q7FNE2_ORYSA
2	1942.5	99.5	369	2	Q9FMQ3_ORYSA
3	1938.5	99.3	369	2	Q9AXF2_ORYSA
4	1927.5	98.7	369	2	Q9FSE6_ORYSA
5	1878.5	96.2	357	2	Q8GZ23_ORYSA
6	1837	94.1	370	2	Q4QWQ7_SACOP
7	1819.5	93.2	369	2	Q43379_AVEA
8	1812.5	92.8	369	2	Q81599_WHEAT
9	1774	90.8	406	2	Q9ZWJ6_MAIZE
10	1519.5	77.8	371	2	Q5K604_SOYBN
11	1505.5	77.1	371	2	Q9M6S1_PEA
12	1504.5	77.0	371	2	Q24077_MEDSA
13	1481.5	75.9	375	2	Q8W406_TOBAC
14	1480.5	75.8	370	2	Q51V18_BRANA
15	1477.5	75.7	373	2	Q84M14_LYCES
16	1476.5	75.6	376	2	Q8H0B4_NICBE
17	1472.5	75.4	370	1	MPK3_ARATH
18	1472.5	75.4	375	2	Q40598_TOBAC
19	1464.5	75.0	369	2	Q5PZV2_9ERAS
20	1461.5	74.8	375	2	Q9LKK2_CAPAN
21	1453.5	74.4	396	2	Q7Y1Y6_LYCES
22	1453	74.4	407	2	Q4JXA8_9CARY
23	1452.5	74.4	396	2	Q84M16_LYCES
24	1448.5	74.2	396	2	Q8LTI8_SOLTU
25	1448	74.1	387	1	MMK1_MEDSA
26	1445.5	74.0	393	1	NTF4_TOBAC
27	1445	74.0	389	2	Q9M534_EUPHOB
28	1442.5	73.9	391	2	Q5K6N6_SOYBN
29	1442	73.8	395	1	MPK6_ARATH
30	1441.5	73.8	371	2	Q04694_PETCR
31	1441.5	73.8	394	2	Q84M15_LYCES

32	1438.5	73.7	393	2	Q04362_TOBAC	Q04362 nicotiana t
33	1438	73.6	403	2	Q683Y6_9MAGN	Q683y6 papaver rho
34	1437.5	73.6	394	2	Q8LTI7_SOLTU	Q8lti7 solanum tub
35	1437	73.6	394	1	MAPK_PEA	Q06060 pisum sativ
36	1436.5	73.6	393	2	Q8H0B3_NICBE	Q8h0b3 nicotiana b
37	1432.5	73.3	398	2	Q84U15_ORYSA	Q84u15 oryza sativ
38	1430	73.2	365	2	Q9XGY8_IPOBA	Q9xgy8 ipomoea bat
39	1426	73.0	387	2	Q84XZ7_PETCR	Q84xz7 petroselinu
40	1421.5	72.8	370	2	Q84XZ5_PETCR	Q84xz5 petroselinu
41	1421.5	72.8	394	2	Q9LKK2_CAPAN	Q9lkk2 capsicum an
42	1415	72.5	403	2	Q84XZ3_WHEAT	Q84xz3 triticum ae
43	1396.5	71.5	399	2	Q9ZWJ5_MAIZE	Q9zwj5 zea mays (m
44	1334.5	68.3	265	2	Q8S3T6_ORYSA	Q8s3t6 oryza sativ
45	1334.5	68.3	392	2	Q6ZD93_ORYSA	Q6z493 oryza sativ

ALIGNMENTS

RESULT 1

Q7FNE2_ORYSA
ID Q7FNE2_ORYSA PRELIMINARY; PRT; 369 AA.
AC Q7FNE2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MAP Kinase.
GN Name=mrsmk2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Leaf;
RC MEDLINE-22069893; PubMed-12074577; DOI=10.1016/S0006-291X(02)00571-5;
RA Agrawal G.K., Rakwal R., Iwahashi H.;
RT "Isolation of novel rice (Oryza sativa L.) multiple stress responsive
MAP kinase gene, OsmSRMK2, whose mRNA accumulates rapidly in response
to environmental cues."
RL Biochem. Biophys. Res. Commun. 294:1009-1016(2002).
DR EMBL; AY486975; CAD31224.1; -; mRNA.
DR HSSP; P24941; IB38.
DR Gramene; Q7FNE2; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004668; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR00719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin_AS.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR001245; Tyr pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 369 AA; 42995 MW; 417081732635P2D3 CRC64;

Query Match 99.5%; Score 1942.5; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 2.9e-113;
Matches 368; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MDGAPVAEFPRTWTHGGRYLIDIFGNKFEVTKYQPPIMPGRGAYGVCSVMNPETRE 60

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Db      1 MDGAPVAFRPTMTHTGGRYLLYDIFGNKFEVNTKYQPPIMPGRGAYGIVCSVMNFETRE 60
Qy      61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120
Db      61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120
Qy      121 DTDLHHIIRSNQELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180
Db      121 DTDLHHIIRSNQELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180
Qy      181 FGLARPSSESDDMTTEVTVTRWYRAPELLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239
Db      181 FGLARPSSESDDMTTEVTVTRWYRAPELLNSTDYSAAIDVMSVGCIFMELINRQPLFPGR 240
Qy      240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
Db      241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300
Qy      300 RMLTFNPLQRIITVEEALDHPYLERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEA 359
Db      301 RMLTFNPLQRIITVEEALDHPYLERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEA 360
Qy      360 IEMNPNIY 368
Db      361 IEMNPNIY 369

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RESULT 2

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Q9FQM3_ORYSA
ID Q9FQM3_ORYSA PRELIMINARY; PRT; 369 AA.
AC Q9FQM3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE MAP kinase 1 (MAP kinase MAPK5a).
GN Name=MAPK5;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22167320; PubMed=12177502; DOI=10.1104/pp.006072;
RA Wen J.Q., Oono K., Imai R.;
RT "Two novel mitogen-activated protein signaling components, OsMEK1 and
RT OsMAP1, are involved in a moderate low-temperature signaling pathway
RT in rice.";
RL Plant Physiol. 129:1880-1891(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22503591; PubMed=12615946; DOI=10.1105/ltpc.008714;
RA Xiong L., Yang Y.;
RT "Disease resistance and abiotic stress tolerance in rice are inversely
RT modulated by an abscisic acid-inducible mitogen-activated protein
RT kinase.";
RL Plant Cell 15:745-759(2003).
DR EMBL; A2216315; AGA40579.1; -; mRNA.
DR EMBL; AF479883; AAL87689.1; -; mRNA.
DR HSSP; Q16539; 1KV1.
DR Gramene; Q9FQM3; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR0003527; MAP kin.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.

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DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 369 AA; 42995 MW; 417D81732635F2D3 CRC64;
Query Match 99.5%; Score 1942.5; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 2.9e-113;
Matches 368; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MDGAPVAFRPTMTHTGGRYLLYDIFGNKFEVNTKYQPPIMPGRGAYGIVCSVMNFETRE 60
Db 1 MDGAPVAFRPTMTHTGGRYLLYDIFGNKFEVNTKYQPPIMPGRGAYGIVCSVMNFETRE 60
Qy 61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120
Db 61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120
Qy 121 DTDLHHIIRSNQELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180
Db 121 DTDLHHIIRSNQELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180
Qy 181 FGLARPSSESDDMTTEVTVTRWYRAPELLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239
Db 181 FGLARPSSESDDMTTEVTVTRWYRAPELLNSTDYSAAIDVMSVGCIFMELINRQPLFPGR 240
Qy 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
Db 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300
Qy 300 RMLTFNPLQRIITVEEALDHPYLERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEA 359
Db 301 RMLTFNPLQRIITVEEALDHPYLERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEA 360
Qy 360 IEMNPNIY 368
Db 361 IEMNPNIY 369
RESULT 3
Q9AXF2_ORYSA
ID Q9AXF2_ORYSA PRELIMINARY; PRT; 369 AA.
AC Q9AXF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAP kinase BINK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song F., Goodman R.M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332873; AAK01710.1; -; mRNA.
DR HSSP; Q16539; 1KV1.
DR Gramene; Q9AXF2; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR003527; MAP kin.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.

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DR PRODOM; PD000001; Prot_kinase; 2.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS001351; MAPK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Kinase.
 SQ SEQUENCE 369 AA; 43029 MW; 417D88E32635FD3D3 CRC64;

Query Match 99.3%; Score 1938.5; DB 2; Length 369;
 Best Local Similarity 99.5%; Pred. No. 5.1e-113;
 Matches 367; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPICRGAYGIVCSVMNPFETRE 60
 DB 1 MDGAPVAEPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPICRGAYGIVCSVMNPFETRE 60

QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHDHENIIGIRDVIPPPIQAFNDVVIATELM 120
 DB 61 MVAIKKIANAFNNDMDAKRTLRKILRLHDHENIIGIRDVIPPPIQAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180
 DB 121 DTDLHHIIRSNQELSEHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMTETVYVTRWYRAPELLNSTDYSAA-DWVSVCICFMELINRQPLPGR 239
 DB 181 FGLARPSSESDMTETVYVTRWYRAPELLNSTDYSAAIDWVSVCICFMELINRQPLPGR 240

QY 240 DHMQHRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
 DB 241 DHMQHRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300

QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDADEPICLEPSPDFEQKALNEDQMQLIFNEA 359
 DB 301 RMLTFNPLQRIITVEEALDHPYLERLHDADEPICLEPSPDFEQKALNEDQMQLIFNEA 360

QY 360 IENNPRIY 368
 DB 361 IENNPRIY 369

RESULT 4

Q9FSE6 ORYSA
 ID Q9FSE6 ORYSA PRELIMINARY; PRT; 369 AA.
 AC Q9FSE6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MAPK2 protein.
 GN Name=mapk2;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Huang H.J., Dai Y.H., Huang D.D., Kuo T.T.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ250311; CAC13967.1; -; mRNA.
 DR HSP; Q16539; 1KV1.
 DR Gramene; Q9FSE6; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004707; F:MAP kinase activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR008351; JNK MAPK.
 DR InterPro; IPR003527; MAP kin.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.

RESULT 5

Q8GZ23 ORYSA
 ID Q8GZ23 ORYSA PRELIMINARY; PRT; 357 AA.
 AC Q8GZ23;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative MAP kinase 1.
 GN Name=OSJNBa0013D02.9;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
 RA Collura K.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC134232; AAO16999.1; -; Genomic DNA.
 DR HSP; Q16539; 1KV1.
 DR Gramene; Q8GZ23; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004707; F:MAP kinase activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR008351; JNK MAPK.
 DR InterPro; IPR003527; MAP kin.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.

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DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 357 AA; 41723 MW; EF6C054A76B3D8FE CRC64;

Query Match          96.2%; Score 1878.5; DB 2; Length 357;
Best Local Similarity 99.7%; Pred. No. 2.7e-109;
Matches 356; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 13 MTHGGRYLLYDIFGNGKPEVNTKYQPPIMPFGAGYGVCSVMNFETREMVAIKKIANAFN 72
DB 1 MTHGGRYLLYDIFGNGKPEVNTKYQPPIMPFGAGYGVCSVMNFETREMVAIKKIANAFN 60

QY 73 NDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELMDTDLHHIIRSNQ 132
DB 61 NDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELMDTDLHHIIRSNQ 120

QY 133 ELSEEHHCQFLYQLRGLKLYIHSANVHRDLKPSNLLNANCDLKICDFGLARPSSESDM 192
DB 121 ELSEEHHCQFLYQLRGLKLYIHSANVHRDLKPSNLLNANCDLKICDFGLARPSSESDM 180

QY 193 MTEYVVTRVYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGRDHMHOMRLITEV 251
DB 181 MTEYVVTRVYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGRDHMHOMRLITEV 240

QY 252 IGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRIIT 311
DB 241 IGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRIIT 300

QY 312 VBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNEAIEMNPNI 368
DB 301 VBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNEAIEMNPNI 357

RESULT 6
Q4QWQ7_SACOF PRELIMINARY; PRT; 370 AA.
AC Q4QWQ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Mitogen-activated protein kinase.
OS Saccharum officinarum (Sugar cane).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC PACCAD clade; Panicoidae; Andropogoneae; Saccharum;
OC Saccharum officinarum complex.
OX NCBI_TaxID=4547;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Noqueira P.T.S., Schlogl P.S., Camargo S.R., Fernandez J.H.,
De Rosa V.E. Jr., Pompermayr P., Arruda P.;
RT "SsNC23, a member of the NAC domain protein family, is associated
with cold, herbivory and water stress in sugarcane.";
RL Plant Sci. 169:93-106(2005).
DR EMBL; AV738652; AAW65993.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 370 AA; 43038 MW; F1C9F29B30A409E CRC64;

Query Match          94.1%; Score 1837; DB 2; Length 370;
Best Local Similarity 94.1%; Pred. No. 1.1e-106;
Matches 348; Conservative 11; Mismatches 9; Indels 2; Gaps 2;

QY 1 MDGAPVAEPRPTWTHGGRYLLYDIFGNGKPEVNTKYQPPIMPFGAGYGVCSVMNFETRE 60
DB 1 MDGAPVAEPRPTWTHGGRYLLYDIFGNGKPEVNTKYQPPIMPFGAGYGVCSVMNFETRE 60

QY 61 MVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELM 120
DB 61 MVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEEHHCQFLYQLRGLKLYIHSANVHRDLKPSNLLNANCDLKICD 180
DB 121 DTDLHHIIRSNQELSEEHHCQFLYQLRGLKLYIHSANVHRDLKPSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMTTEYVVTRVYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGR 239
DB 181 FGLARPSSESDMTTEYVVTRVYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGR 240

QY 240 DHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLI 298
DB 241 DHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLI 300

QY 299 ERMILTFNPLQRIITVBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNE 358
DB 301 ERMILTFNPLQRIITVBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNE 360

QY 359 AIEMNPNI 368
DB 361 AIEMNPNI 370

RESULT 7
Q43379_AVESA PRELIMINARY; PRT; 369 AA.
AC Q43379;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE MAP KINASE.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Avenaeae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huttly A.K., Phillips A.L.;
RT "gibberellin regulated expression in oat aleurone cells of two kinases
that have homology to nap kinase and a ribosomal protein kinase.";
RL Plant Mol. Biol. 27:1043-1052(1995).
DR EMBL; X79993; CAA56314.1; -; mRNA.
DR PIR; S56638; S56638.
DR HSSP; Q16539; 1KV1.
DR Gramene; Q43379; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 369 AA; 42871 MW; 2A76A350A867A63F CRC64;

Query Match          93.2%; Score 1819.5; DB 2; Length 369;
Best Local Similarity 91.3%; Pred. No. 1.3e-105;

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Matches 337; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTHGGRVLLYDIFGNKEFTVNTKYQPPIMPGRGAYGIVCSVMNPETRE 60
 DB 1 MDGAPVAEPRPTMTHGGRVLLYDIFGNKEFTVNTKYQPPIMPGRGAYGIVCSVMNPETRE 60

QY 61 MVAIKKIANAFNDMDAKETLREIKLLRHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120
 DB 61 MVAIKKIANAFNDMDAKETLREIKLLRHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180
 DB 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGR 239
 DB 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGR 240

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 299
 DB 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 300

QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 359
 DB 301 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 360

QY 360 IEMNPNIY 368
 DB 361 LELNPNFNY 369

RESULT 8
 O81599 WHEAT
 ID O81599 WHEAT PRELIMINARY; PRT; 369 AA.
 AC O81599;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MAP kinase homolog.
 GN Names=WCK-1;
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Chihokukomugi;
 RX MEDLINE=99454541; PubMed=10527417; DOI=10.1023/A:1006263607135;
 RA Takezawa D.;
 RT "Elicitor- and A23187-induced expression of WCK-1, a gene encoding
 RT mitogen-activated protein kinase in wheat.";
 RL Plant Mol. Biol. 40: 921-933 (1999).
 DR EMBL; AF079318; AAC28850.1; -; mRNA.
 DR HSP; Q16539; IKV1.
 DR Gramene; O81599; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004707; F:MAP kinase activity; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR008351; JNK_MAPK.
 DR InterPro; IPR003527; MAP_Kin.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR InterPro; IPR002290; Ser Thr_pkinase.
 DR Pfam; PF00069; Pkinase; I.
 DR PRINTS; PR01772; JNKMAPKINASE.
 DR ProDom; PD000001; Prot kinase; 2.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS01351; MAPK; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Kinase.

SQ SEQUENCE 369 AA; 42803 MW; D8DD351176978434 CRC64;

Query Match 92.8%; Score 1812.5; DB 2; Length 369;
 Best Local Similarity 91.1%; Pred. No. 3.7e-105;
 Matches 336; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTHGGRVLLYDIFGNKEFTVNTKYQPPIMPGRGAYGIVCSVMNPETRE 60
 DB 1 MDGAPVAEPRPTMTHGGRVLLYDIFGNKEFTVNTKYQPPIMPGRGAYGIVCSVMNPETRE 60

QY 61 MVAIKKIANAFNDMDAKETLREIKLLRHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120
 DB 61 MVAIKKIANAFNDMDAKETLREIKLLRHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180
 DB 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGR 239
 DB 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGR 240

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 299
 DB 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 300

QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 359
 DB 301 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 360

QY 360 IEMNPNIY 368
 DB 361 LELNPNFNY 369

RESULT 9
 Q9ZMJ6 MAIZE
 ID Q9ZMJ6 MAIZE PRELIMINARY; PRT; 406 AA.
 AC Q9ZMJ6;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MAP kinase 4.
 GN Names=ZmMPK4;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OC NCBI_TaxID=4577;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=honeybuntam;
 RX MEDLINE=20055759; PubMed=10589842; DOI=10.1007/s004380051115;
 RA Berberich T., Sano H., Kusano T.;
 RT "Involvement of a MAP kinase, ZmMPK5, in senescence and recovery from
 RT low-temperature stress in maize.";
 RL Mol. Gen. Genet. 262:534-542 (1999).
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 DR EMBL; AB016801; BAA74733.1; -; mRNA.
 DR HSP; Q16539; IKV1.
 DR Gramene; Q9ZMJ6; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004707; F:MAP kinase activity; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR008351; JNK_MAPK.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR InterPro; IPR002290; Ser Thr_pkinase.
 DR Pfam; PF00069; Pkinase; I.
 DR PRINTS; PR01772; JNKMAPKINASE.
 DR ProDom; PD000001; Prot kinase; 2.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS01351; MAPK; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Kinase.

DR	ProDom; PD000001; Prot_kinase; 2.
DR	SMART; SMO0220; S_TK; 1.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW	ATP-binding; Kinase; Nucleotide-Binding;
KW	Serine/threonine-protein kinase; Transferase.
SQ	SEQUENCE 406 AA; 46683 MW; E63A60A5C102A3F1 CRC64;
Query Match	
Best Local Similarity 90.8%; Score 1774; DB 2; Length 406;	
Matches 33; Conservative 18; Mismatches 13; Indels 32; Gaps 3	
Qy	1 MDGA-PAVEPRFTTHGGRYLLYDIFGNKFVETNKYQPIMPICRGAYGIVCSVMNFETR 59 : : : : : : : : : : : : : : :
Dd	7 MDGSPVAEPQTTVTHGGRLRYNIFGNLFETIRKYQPPVMPICRGAYGIVCSVMNFETR 66 : : : : : : : : : : : : : : :
Qy	60 EMVAIKKIANAFAFNMDMAKPTLREIKLRHLRHDHENIIGIRDVIPIPPPOAFNDVVIATEL 119 : : : : : : : : : : : : : : :
Dd	67 EMVAIKKIANAFAFNHMDAKRTLREIKLRHLRHDHENIIGIRDVIPIPPVQAFNDVVIATEL 126 : : : : : : : : : : : : : : :
Qy	120 MDTDLHHIIRSNQELIREHCQVFYLQILRGUKYIHSAHVHRDLKPSNLLANNCDAKIC 179 : : : : : : : : : : : : : : :
Dd	127 MDTDLHHIIRSNQELISEHSQVFYLQILRGUKYIHSAHVHVDLKPSNLLVANCDLKIC 186 : : : : : : : : : : : : : : :
Qy	180 DFLGARPSSESDMMTEYVVTRYRAPELLLNSTDYSAA-DVWSVCIFMELINROPLFPFG 238 : : : : : : : : : : : : : : :
Dd	187 DFLGARPSSESDMMTEYVVTRYRAPELLLNSTDYSAAIDVWSVCIFMELINROPLFPFG 246 : : : : : : : : : : : : : : :
Qy	239 RDHMHWMLRLITE-----VIGTPTDDELGLFIERNEDA 268 : : : : : : : : : : : : : : :
Dd	247 RDHMHWMLRLTEARVTHTATPTSPSYNSIPSSSAHNIAARQVIGTPTDDELGLFIERNEDA 306 : : : : : : : : : : : : : : :
Qy	269 RKYWEHLPOYPRTTFASMFPPVQAALDLIERMLTFNPLOKITVEEALDHVPYLERLHDIA 328 : : : : : : : : : : : : : : :
Dd	307 RKYMRHLUPQFRPRRFVSFLFPMQPVALLDLIERMLTFNPLOKITVEEALHPYLERLHDVA 366 : : : : : : : : : : : : : : :
Qy	329 DEPICLPFFSDFEQKALNEQDKQLIFNEAIEMNNPIRY 368 : : : : : : : : : : : : : : :
Dd	367 DEPICTPFPSDFEQQALTEQDKQLIFNEAIENPNFERY 406 : : : : : : : : : : : : : : :
RESULT 10	
QSK6Q4_SOYBN	
ID	QSK6Q4_SOYBN PRELIMINARY; PRT; 371 AA.
AC	QSK6Q4
DT	10-MAY-2005 (TrEMBLrel. 30, Created)
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE	Mitogen-activated protein kinase 1.
GN	Name=WPK1;
OS	Glycine max (Soybean).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX	NCBI_TaxID=3847;
RN	[1]
NUCLEOTIDE SEQUENCE.	
RP	Daxberger A., Mitchofer A., Nemak A., Hirt H., Ebel J.;
RT	"elictor-activated mitogen-activated protein kinase(s) (MAPK) from soybean (Glycine max L.)";
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF104247; AAQ13491.1; -, mRNA.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004707; F:MAP kinase activity; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR	InterPro; IPRO08351; JNK_MAPK.
DR	InterPro; IPRO03527; MAP_kin.
DR	InterPro; IPRO00719; Prot.kinase.
DR	InterPro; IPRO02290; Ser_thr_pkinase.
DR	InterPro; IPRO08271; Ser_thr_pkin AS.

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DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR01772; JNKMAPKINASE.
DR ProDom: PD000001; Prot kinase; 2.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 371 AA; 42919 MW; A6F422D295CF488C CRC64;

Query Match 77.1%; Score 1505.5; DB 2; Length 371;
Best Local Similarity 74.7%; Pred. No. 5e-86;
Matches 269; Conservative 55; Mismatches 35; Indels 1; Gaps 1;

QY 6 VAEFRPTMTGGRYLLDYIFGNKFEVTKYQPPIMPPIGRGAYGIVCSVMNFETREMVAK 65
DB 9 VAEFPVQTHGGQFQVNVFGNLFVETAKYRPPIMPPIGRGAYGIVCSLLNTETNELVAK 69
QY 66 KIANAFNNDMDAKRTLEIKLRLHLDHENIIGIRDVIPPPIQAFNDVVIATLMDTDLH 125
DB 69 KIANAFDNHMDAKRTLEIKLRLHLDHENVIGLRDVIPLPREFNDVITTELMDTDLH 128
QY 126 HIIRSNQELSEHCQFYLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKI CDFGLAR 185
DB 129 QIIRSNQNLSDERHCQFYLYQLRGLRYIHSANIIHRDLKPSNLLNANCDLKI CDFGLAR 188
QY 186 PSESMDMTYVYVTRWRAPPELLNSTDY- SAADVMSVGCIFMELNINROPLPGRDHMQ 244
DB 189 PTMENDFMTEYVYVTRWRAPPELLNSTDYSAIDVMSVGCIFMELNKKPLPFGKDHVHQ 248
QY 245 MRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDIERMILTF 304
DB 249 MRLITELLGTPTDADVLGVKNEDARRYIRQLPOYPRQLNRPVPHVPLAIDLIDKMLTI 308
QY 305 NPLQRTITVEALDHPYLERLHDIADPEPICLEPSPDFEQKALNEDQMKQLIFNEAITEMNP 364
DB 309 DPTRRITVEALAHPLYLEKLDHVADEPICMEPSPDFEQKHLDEEQIKEMIVREALANLP 368

RESULT 12
O24077 MEDSA
ID O24077_MEDSA PRELIMINARY; PRT; 371 AA.
AC O24077;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase.
GN Name=MKK4;
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
OC Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97008170; PubMed=8855346; DOI=10.1073/pnas.93.20.11274;
R Jonak C., Kiegiel S., Ligtnering W., Barker P., Huskinson N., Hirt H.;
RT "signaling in plants: a mitogen-activated protein kinase pathway is
RL activated by cold and drought."
R Proc. Natl. Acad. Sci. U.S.A. 93:11274-11279(1996).
DR EMBL: X82270; CAA57721.1; -, mRNA.
DR FRR; T09622; T09622.
DR HSP; Q16539; IKV1.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004707; F:MAP kinase activity; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR008351; JNK MAPK.
DR InterPro: IPR003527; MAP_kin.

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DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR01772; JNKMAPKINASE.
DR ProDom: PD000001; Prot kinase; 2.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 371 AA; 42963 MW; 8CCC390454E4350E CRC64;

Query Match 77.0%; Score 1504.5; DB 2; Length 371;
Best Local Similarity 74.4%; Pred. No. 5.8e-86;
Matches 268; Conservative 56; Mismatches 35; Indels 1; Gaps 1;

QY 6 VAEFRPTMTGGRYLLDYIFGNKFEVTKYQPPIMPPIGRGAYGIVCSVMNFETREMVAK 65
DB 9 VAEFPVQTHGGQFQVNVFGNLFVETAKYRPPIMPPIGRGAYGIVCSLLNTETNELVAK 69
QY 66 KIANAFNNDMDAKRTLEIKLRLHLDHENIIGIRDVIPPPIQAFNDVVIATLMDTDLH 125
DB 69 KIANAFDNHMDAKRTLEIKLRLHLDHENVIGLRDVIPLPREFNDVITTELMDTDLH 128
QY 126 HIIRSNQELSEHCQFYLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKI CDFGLAR 185
DB 129 QIIRSNQNLSDERHCQFYLYQLRGLRYIHSANIIHRDLKPSNLLNANCDLKI CDFGLAR 188
QY 186 PSESMDMTYVYVTRWRAPPELLNSTDY- SAADVMSVGCIFMELNINROPLPGRDHMQ 244
DB 189 PTMENDFMTEYVYVTRWRAPPELLNSTDYSAIDVMSVGCIFMELNKKPLPFGKDHVHQ 248
QY 245 MRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDIERMILTF 304
DB 249 MRLITELLGTPTDADVLGVKNEDARRYIRQLPOYPRQLNRPVPHVPLAIDLIDKMLTI 308
QY 305 NPLQRTITVEALDHPYLERLHDIADPEPICLEPSPDFEQKALNEDQMKQLIFNEAITEMNP 364
DB 309 DPTRRITVEALAHPLYLEKLDHVADEPICMEPSPDFEQKHLDEEQIKEMIVREALANLP 368

RESULT 13
Q8W406 TOBAC
ID Q8W406_TOBAC PRELIMINARY; PRT; 375 AA.
AC Q8W406;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Wound induced protein kinase.
GN Name=WIPK;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sano H., Yap Y.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AB052964; BAB79636.1; -, Genomic_DNA.
DR HSP; Q16539; IKV1.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004707; F:MAP kinase activity; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR008352; p38_MAPK.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.

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DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01773; P38MAPKINASE.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 375 AA; 42898 MW; 9BA49C839E1C88F CRC64;

Query Match 75.9%; Score 1481.5; DB 2; Length 375;
Best Local Similarity 73.0%; Pred. No. 1.6e-84;
Matches 265; Conservative 55; Mismatches 42; Indels 1; Gaps 1;

QY 3 GAPVAEPRPTWTHGGRYLLYDIFGNKFEVTKYQPPIMPGRGAYGIVCSVMNFEETREMV 62
DB 10 GGQFPDPFSLVTHGGYQYDIFGNFETTKYRPPIMPGRGAYGIVCSVLNTELMNV 69
QY 63 AIKKIANAFNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELMDT 122
DB 70 AVKIANAFNDYMDAKRTLREIKLRLHLDHENVIGLRDVIPLRLREFSDVVIATELMDT 129
QY 123 DLHIIIRSNQELSEHCQFLYQILRGKYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 130 DLHQIIRSNQGLSEHCQFLYQILRGKYIHSANVLRDLKPSNLLNANCDLKICDPG 189
QY 183 LARPSSEDMTEYVTVRYRAPELLNSTDYSA-DVWSGCI FMEILNRPLPGRDH 241
DB 190 LARPNIENEMTEYVTVRYRAPELLNSTDYTAIDVWSGCI FMEILNRKPLFAGKDH 249
QY 242 MHQRLITVEIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIERM 301
DB 250 VHQIRLLTFTGTPTEADLGFQNEADAKYIYQLPQHPQQLAEVPPHVNPLAIDLVDKM 309
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADPICLEPSPDFEQKALNEDQMQLIFNEAIE 361
DB 310 LTLDPFRRITVEALDHPYLERLHDIADPICLEPSPDFEQKALNEDQMQLIFNEAIE 369
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DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mitogen-activated protein kinase 3.
OS Brassica napus (Rapel).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yu S., Zhang L., Zuo K., Tang D., Tang K.;
RT "Isolation and characterization of an oilseed rape MAP kinase BnMPK3
RT involved in diverse environmental stresses.";
RL Plant Sci. 169:413-421(2005).
DR EMBL; AY642433; RAV34677.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008350; Erk 3 4 MAPK.
DR InterPro; IPR008351; JNK_MAPK.
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DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01771; ERK3ERK4MAPK.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 370 AA; 42594 MW; 84C29502FCB167B9 CRC64;

Query Match 75.8%; Score 1480.5; DB 2; Length 370;
Best Local Similarity 73.8%; Pred. No. 1.8e-84;
Matches 268; Conservative 54; Mismatches 40; Indels 1; Gaps 1;

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DB 185 LARPSENEFTEYVTVRYRAPELLNSTDYTAIDVWSGCI FMEILNRKPLPFGKDH 244
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QY 302 LTFNPLQRIITVEALDHPYLERLHDIADPICLEPSPDFEQKALNEDQMQLIFNEAIE 361
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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GN Name=MPK3;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22795301; PubMed=12913131; DOI=10.1104/pp.103.024414;
RA Holley S.R., Yamanchili R.D., Moura D.S., Ryan C.A., Stratmann J.W.;
RT "Convergence of signaling pathways induced by systemin,
RT oligosaccharide elicitors, and ultraviolet-B radiation at the level of
RT mitogen-activated protein kinases in Lycopersicon peruvianum
RT suspension-cultured cells.";
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Job time : 233 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 29, 2005, 04:41:30 ; Search time 4041 Seconds
(without alignments)
16163.021 Million cell updates/sec

Title: US-10-768-886-1
Perfect score: 1396
Sequence: 1 agagagtcagataaggtcgt.....ttaaaaaaaaaaaaaaaaaa 1396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
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5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1072.4	76.8	1074	10	CL961355
2	755	54.1	755	6	CB675228
3	748.8	53.6	752	6	CB675229
4	725	51.9	1031	7	CK163044
5	668.2	47.9	863	2	BE412950
6	663.2	47.5	916	3	BM817317
7	654.6	46.9	921	8	DR792177
8	623.2	44.6	859	7	CN130436
9	611.4	43.8	718	6	CA213307
10	608	43.6	632	7	CK077805
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14	594.2	42.6	667	3	BI805515
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16	590.8	42.3	806	7	CO527096
17	589	42.2	1152	8	DR741482
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19	578.4	41.4	949	6	CA150824
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	26	560.8	40.2	768	6	CA159385
	27	559.4	40.1	783	8	DR787175
	28	555.4	39.8	857	7	CN130591
	29	550	39.4	1004	7	CO731261
	30	549	39.3	775	8	DR813762
	31	547.4	39.2	590	7	CR292974
	32	546	39.1	675	7	CV071886
	33	541.6	38.8	819	7	CK199849
	34	536.6	38.4	600	6	CA484243
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	40	524.2	37.6	835	7	CK201815
	41	522.6	37.4	695	2	BF622856
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ALIGNMENTS

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DEFINITION OsIFCC006088 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL961355
VERSION CL961355.1 GI:52377449
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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/mol_type="genomic DNA"
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RESULT 2

CB675228

LOCUS

CB675228

755 bp

mRNA

linear

EST 09-APR-2003

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DEFINITION OSJNEe10N07.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEe10N07 5', mRNA sequence.
ACCESSION CB675228
VERSION CB675228.1 GI:29678953
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 755)
AUTHORS Jantassuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 15886893
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
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RESULT 3
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

CB675229 752 bp mRNA linear EST 09-APR-2003
OSJNBe10N07 3', mRNA sequence.
CB675229 1 GI:29678954
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristaceae; Oryzaceae; Oryza.
Jantassuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
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FORWARD: gta aaa cga cgg cca gtc
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SOURCE
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XhoI; 24 hrs after inoculation with Rice Blast (70-15)"
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Db 332 CTTAGAGATGTCACGACATCGCCGATGAGCCCATCTGCTGAGGAGCTTCTCTTCGA 273
QY 1100 CTTGAGGAGGAGGCTCTTAAACGAGGACCAAAATGAAGAGCTGATCTTCAACGAAGCAT 1159
Db 272 CTTGAGGAGGAGGCTCTTAAACGAGGACCAAAATGAAGAGCTGATCTTCAACGAAGCAT 213
QY 1160 CGAGATGAACCCAAACATCGGTTACTAGATTGAATCAACATGGAATGAGATCCCGTCTA 1219
Db 212 CGAGATGAACCCAAACATCGGTTACTAGATTGAATCAACATGGAATGAGATCCCGTCTA 153
QY 1220 TACCTGCTTTGTATATATGATCAAGATTGAGAGCCGGGTAGATGAACATGATTTGTT 1279
Db 152 TACCTGCTTTGTATATATGATCAAGATTGAGAGCCGGGTAGATGAACATGATTTGTT 93
QY 1280 TGTGTTGATGTTTGAACCCGACATCTCTCAAGTTGCTGCTGCTTCTGATGATATAT 1339
Db 92 TGTGTTGATGTTTGAACCCGACATCTCTCTCAAGTTGCTGCTGCTTCTGATGATATAT 33
QY 1340 GGTACTATGTTTGAATTAAGAGGCTTTGGAAT 1371
Db 32 GGTACTATGTTTGAATTAAGAGGCTTTGGAAT 1

CK163044 1031 bp mRNA linear EST 05-DEC-2003
FGAS015659 Triticum aestivum FGAS: Library 4 Gate 8 Triticum
aestivum cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaceae; Triticum.

REFERENCE
AUTHORS
Allard, F., Crosby, W.D., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
1 (bases 1 to 131)
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroché, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J. L. and Sarhan, F.
1 (bases 1 to 131)

Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.estcs@usask.ca
This sequence is the direct result of the Base calling software
phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [40,815].
Plate: L4B006 row: 0 column: 18.

FEATURES

1. :1031
organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;
Conditions for growth: Seeds were germinated in a
water-saturated mix (50% black earth and 50% ProMix) in a
growth chamber for 7 days under an irradiance of 200 mmol
m⁻² sec⁻¹. The temperature was maintained at 20 degrees C
with a 15-hr photoperiod under a relative humidity of 70%.
After this period watering of plants was stopped. Four
time points were sampled during a two week period; the
first after wilting was observed and the last, two weeks
later, consisted of live crown and leaf tissue (leaf
tissue that was yellow was not included in sampled
material). First strand synthesis in this library was done
in the presence of methylated dCTP thereby protecting from
internal cleavage with NotI."

ORIGIN

Query Match	51.9%	Score	725;	DB	7;	Length	1031;		
Best Local Similarity	88.0%	Prod. No.	1e-158;						
Matches	821;	Conservative	0;	Mismatches	109;	Indels	3;	Gaps	3
Qy	53	GAGAGAGAGGAGGAGATTAGGAGTGGAGCGGGCGCGCGTGGCGGAGTTTCAGGCCGAC	112						
Db	99	GAGAGTTTCTTGGCTGTGTTTGGAGAATGGACGGCGCTCCGGTGGCCGAGTTTCCGCCCCGAC	158						
Qy	113	GATGACGACGCGCGGCCGCTACTGCTCTACGACATCTTCGGGAACAAGTTTCGAGGTGAC	172						
Db	159	GATGACGACGCGCGGCCGCTCTCTCTCTACAAATATTCGGCAACAGTTTCGAGATCAC	218						
Qy	173	GAAACAAGTACAGCGGCCCATCATGCCCCATTGGCCGCGCGCCTACGGGATGCTCTGCTC	232						
Db	219	GGCCAAAGTACCAGCGCCCGATCATGCCCATCGCCGCGCGCTACGGGATCGTCTGCTC	278						
Qy	233	CGTGATGAACTTTGAGACGAGGAGATGGTGGCGATAAAGAGATCGCCACCGCGTTCAA	292						
Db	279	GGTGATGAACCTTCGAGACGAGGGAGATGGTGGCAATCAAGAAGATCGCAAAACGCTTTTCCA	338						
Qy	293	CAACGACATGACGCGCAAGCGCACGCTCCGGGAGATCAAGCTCTCCAGGCACCTCGACCA	352						
Db	339	CNAACAACTGACGCGCAAGCGCACGCTCCGGGAGATCAAGTCTCTAGAGCACTTCGACCA	398						
Qy	353	CGAGAACATCATAGGCATCAGGGATGTGATCCCGCCGCCGATCCCTCAGGGGTTTCAACGA	412						
Db	399	CGAGAACATAGTGGCTTCGAGATGTGATCCCGCCGCCGACCCCGCAGTCTCTTCAACGA	458						

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FEATURES
  source      Location/Qualifiers
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  /db_xref="taxon:4513"
  /clone="MCG016.H09"
  /tissue_type="leaf/culm"
  /dev_stage="etiolated"
  /clone_lib="rTEC MCG Barley Leaf/culm Library"

ORIGIN
Query Match      47.9%; Score 668.2; DB 2; Length 863;
Best Local Similarity 89.6%; Pred. No. 2e-145;
Matches 715; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 219 GGGATCGTCTGCTCCGATGAATTTGAGACAGGAGAGATGTTGGCGATAAAGAGATC 278
Db 17 GGNATCGTCTGCTCGGTGATGAATTCGACAGGAGAGATGNGGCAATCAAGAAGATC 76
QY 279 GCCAACGGCTTCAACAACGACATGAGCGCCCAAGCGACGCTCCGGGAGATCAAGTCTCTC 338
Db 77 GCAACGGCTTGCACACAAACATGGAGCGCCCAAGCGACGCTCCGGGAAATCAAACTCTC 136
QY 339 AGGCACCTCGACCAACGAGACATCATAGGCATCAGGATGTGATCCCGCGCGATCCCT 398
Db 137 AAGACCTTCGACCAACGAGAACATAGTAGGCTCCGAGACGTGATCCCGCGCGATCCCG 196
QY 399 CAGGCGTTCAACGACGCTTACATCGCCACGAGGCTCATGACACCGACCTCCCATCATC 458
Db 197 CAGTCTTCAACGAGCTTACATCGCCACTGAGCTCATGACACCGACCTTCAACCATC 256
QY 459 ATCCGCTTCAACCAAGAACTGTGAGAAAGACATGCGCAGTATTTCTGTACCAAGTCTG 518
Db 257 ATCCGCTTCAACCAAGAACTGTGAGAAAGACATGCGCAGTATTTCTGTACCAAGTCTG 316
QY 519 CGGGGCTCAAGTACATCCACTCGGGAAGTGTATCCACGCGACCTGAGCGGAGCAAC 578
Db 317 CGGGGCTCAAGTACATCCACTCGGGAAGTGTATCCACGCGACCTGAGCGGAGCAAC 376
QY 579 CTGCTGTAACGCAACTCGCACTCGCACTTCAAGATCTGCGACTTGGCGCTGGCGCGCGCTG 638
Db 377 CTGCTGTAACGCAACTCGCACTTGGACTTCAAGATCTGCGACTTGGCGCTGGCGCGCGCTG 436
QY 639 TCGGAGAGCGACATGATGACGAGTACGTTGTTACCCGTTGATACCGCGCGCGCGAGCTG 698
Db 437 TCGGAGAGCGACATGATGACGAGTACGTTGTTACCCGTTGATACCGCGCGCGCGAGCTG 496
QY 699 CTGCTCAACTCCACCGACTACTCGCGCGCATCGAGCTGTGTTCCGTCCGCTGCATCTTC 758
Db 497 CTGCTCAACTCCACCGACTACTCGCGCGCATCGAGCTGTGTTCCGTCCGCTGCATCTTC 556
QY 759 ATGAGGCTCATCAACCGCGAGCGCTCTTCCCGGACAGGACCAACATGACAGATCGCG 818
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QY 819 CTATCAACCGAGTGTGGAAGCGCGACCGGACGAGATGAGGTTTATACGGAACGAG 878
Db 617 CTATCAACCGAGTGTGGAAGCGCGACCGGACCGAGATGAGGTTTATACGGAACGAG 676
QY 879 GAGCGAGGAGTACATGAGGACCTTCCGCGAGTACCGCGCGGAGGTTTCGGGAGCATG 938
Db 677 GAGCGAGGAGTACATGAGGACCTTCCGCGAGTACCGCGCGGAGGTTTCGGGAGCATG 736
QY 939 TTCCCGCGGTTGACCGCGCGCTCGACTCATCGAGAGGATGCTCACTTCAACCCG 998
Db 737 TCCCAAGGTGCAAGNCAGCGCGCTCGACTCATAGAGCGGATGCTTACCTTCAACCCG 796
QY 999 CTGAGAGATACAGTT 1016
Db 797 NTTGAGAGGATCACAGT 814

ORIGIN
Query Match      47.5%; Score 663.2; DB 3; Length 916;
Best Local Similarity 88.7%; Pred. No. 3e-144;
Matches 763; Conservative 0; Mismatches 93; Indels 4; Gaps 4;

QY 70 GATTAGGATGGACGGCGCGCGTGGCGAGTTTCAGGCGGATGATGACGACGCGCGCC 129
Db 48 GTTTGAGATGGACGGCGCGTGGCGAGTTTCGGCGGATGATGACGACGCGCGCC 107
QY 130 GGTACTGCTCTACGACATTTTCGGGAACAAGTTTCGAGGTGAGCAACAAGTACGAGCGCC 189
Db 108 GGTTCCTCTCTACAACATATTCGGCAACCAAGTTTCGAGATCAGCGGCAAGTACGAGCGC 167
QY 190 CCATCATGCCATTTGGCGCGCGCTTACGGGATGCTGCTCGGTGATGAATTCAGATCAGA 249
Db 168 CGATCATGCCATTTGGCGCGCGCTTACGGGATGCTGCTCGGTGATGAATTCAGATCAGA 227
QY 250 CGAGGAGATGGTGGCGATTAAGAAGATCGCCAAACGGTTTCAACAACGATGAGCGCCA 309
Db 228 CGAGGAGATGGTGGCGATTAAGAAGATCGCCAAACGGTTTCAACAACGATGAGCGCCA 287
QY 310 AGCGCAAGCTTCGGGAGATCAAGCTCTTCAGGCACTTCGACCAAGCAATCATAGGCA 369
Db 288 AGCGCAAGCTTCGGGAAATCAAACTCTCAAGCACCTTCGACCAAGCAATCATAGGCA 347
QY 370 TCAGGAGTGTATCCCGCGCGCATCCCTCAGGGTTCAACGAGCTTACATGCGCAGG 429
Db 348 TCCGAGACGTGATCCCGCGCGCATCCCTCAGGGTTCTTTCAACGAGCTTACATGCGCAGT 407
QY 430 AGCTCATGGACCGGACCTTCATCATCATCGCTTCCCAACCAAGAACTGTGAGAGAGC 489
Db 408 AGCTCATGGACCGGACCTTCATCATCATCGCTTCCCAACCAAGAACTGTGAGAGAGC 467
```

Qy	490	ACTGCCAGTATTTCTGTGTACAGATCTGCGGGGGCTCAAGTATACATCCACTCGGCGAAGC	549
Db	468	ACTGCCAGTATTTCTGTGTACAGAGTGTGCGGGTCTCAAGTATACATCCACTCGGCGAAGC	527
Qy	550	TGATCCACCGGACCTGAAGCCGAGCAACTGCTGCTGAACGCCCAACTCGGACCTCAAGA	609
Db	528	TGATCCATCGGACCTGAAGCCGAGCAACTGCTGCTGAACGCCCAACTCGGACCTCAAGA	587
Qy	610	TCTGGCACTTCGGGCTGGCGGGCCGTGTCGGAGAGCGACATGATGACGGAGTACGTGG	669
Db	588	TCTGGCACTTCGGGCTGGCGGGCCGTGTCGGAGAGCGACATGATGACGGAGTACGTGG	647
Qy	670	TCACCGGTGTGTACCGCG-CGCGGAGTGTGCTCAACTCCACCGCATCTCTCCGCGGCC	728
Db	648	TCACGCGTGTGTACCGGGCCCCGGAGCTGTGCTCAACTCCACCGCATCTCTCCGCGGCC	707
Qy	729	ATCGACGTCTGGTTCGTGGGTGCACTTTCATGGAGCTCATCAAACGCG-CAGCGGCTCTT	787
Db	708	ATCGACGTCTGGTTCGTGGGTGCACTTTCATGGAGCTCATCAAACGCGGCAACGCGCTCTT	767
Qy	788	CCC CGGACGGGACCACTGCACAGATGCGCTCATCACCGAGGTGATCGGAGACGCCAC	847
Db	768	CCC GGGGAAGGACCCCATGCAACCAAGATGCGCTCATCACGGGAGTATCGGAGACCCCAAC	827
Qy	848	GGACGACGAGCTGGGGTTCA-TACGGAGAGGAGCGGAGGAGTACATGA-GGCACCTGG	905
Db	828	CGACGACACCTTGGGCTTTATTACCGGACGAGGACGCCACGAGATACATGAGGGGCATTTG	887
Qy	906	CCG CAGTACCCGCGCCGAC	925
Db	888	CCGAAGTTCCCTCGTCCGGC	907

[illegible]

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1. (bases 1 to 921)

Kim, H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

```

FEATURES
source
1. .921
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_hosts="DH10B T1 phage resistant"
/clone_lib="ZM BfB"
/note="vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues. Organ: silks,

```

ORIGIN

the University of Arizona
(<http://www.genome.arizona.edu/orders/>)

QY 708 TCACCGACTACTCCGCGCCCATCGAGCTCTGGTCGGCTGCATCTTCATGGAGCTC 767
 DB 784 TCACCGACTACTCCGCGCGCATCGAGCTCTGGTCGGCTGCATCTTCATGGAGCTC 843
 QY 768 ATCAACCGCCAGCGCTCTTCCCGGCGAGGAGCACATGACACAGATGCGCCTCATCACC 827
 DB 844 AATCACCGCCAGCGCTCTTCCCGGCGAGGAGCACATGACACAGATGCGCCTCATACC 903
 QY 828 GAGGTATCGGAGCGCC 844
 DB 904 GAGGTATCGGAGCGCC 920

RESULT 8
 CN130436
 LOCUS
 DEFINITION RHOH1_41_B01.g1_A002 Acid- and alkaline-treated roots Sorghum EST 01-APR-2004
 bicolor cDNA clone RHOH1_41_B01_A002 5', mRNA sequence.

ACCESSION CN130436
 VERSION CN130436.1 GI:45958964
 KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum).

ORGANISM

Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
 An EST database from Sorghum: acid- and alkaline-treated roots
 Unpublished (2003)

TITLE

RHOH1_41_B01.b1_A002

JOURNAL

COMMENT

Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTCG).

FEATURES

source

Location/Qualifiers
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 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /clone="RHOH1_41_B01_A002"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /host="Acid- and alkaline-treated roots"
 /note="Organ: Root; Vector: pME18S-PL3; Site 1: XhoI;
 Site 2: XhoI; The library was prepared from polyA+ RNA
 from 8-day-old roots harvested from BTx623 sorghum
 seedlings grown in hydroponic culture. HCl was added to a
 pH of 3.0 to some seedlings, KOH to a pH of 9.0 for
 others. Roots were harvested 3, 12 and 27 hr after
 addition and pooled for RNA preparation. Double-stranded
 cDNA was cloned unidirectionally into different DraIII
 sites of the pME18S-PL3 vector (5-prime DraIII site is
 CACTGTGTG, 3-prime draIII site is CACCATGTG). XhoI excises
 the cDNA insert."

ORIGIN

Query Match 44.6%; Score 623.2; DB 7; Length 859;
 Best Local Similarity 81.5%; Pred. No. 6.8e-135;
 Matches 782; Conservative 0; Mismatches 73; Indels 105; Gaps 1;

RESULT 9

CA213307

LOCUS

DEFINITION

ACCSSION

VERSION

CA213307
 SCQGSB1140A09.g SB1 Saccharum officinarum cDNA clone SCQGSB1140A09
 5', mRNA sequence.
 CA213307
 CA213307.1 GI:35259472

QY 68 GGGATTAGGGATGGACGGGCGCGGTGGGGAGTTTCAGCGGACGATACCGCACGGCGG 127
 DB 5 GTGAGAGGCATGGACGGAGCTCCGGTCCGGAGTTCCGGCGACGGTACGCGCAACCG 64
 QY 128 CGGTTACCTGCTCTACGACATCTTCGGGAAACAAAGTTTCGAGGTGACCAACAAAGTACAGGCC 187
 DB 65 CGGTTCTTGCAGTACACATCTTCGGCAACCTGTTTCGAGATCAGCGACAAAGTACAGGCC 124
 QY 188 GCCCATCATGTCCTATGCGCGCGCTTACGGGATCGTCTCCGTGATGAATTTGA 247
 DB 125 TCCCATCATGTCCTATGCGCGCTTACGGGATCGTCTCCGTGATGAATTTGA 184
 QY 248 GACGAGGAGATGGTGGCGATTAAGNAGATCGCCACCGTTCAACAAAGCATGCAAGCC 307
 DB 185 GACGAGGAGATGGTGGCGATTAAGNAGATCGCCACCGTTCAACAAAGCATGCAAGCC 244
 QY 308 CAAGCGCAGCTCCGGGAGATCAAGCTCTTCAGGACCTTCGACGAGAGAAATCATAGG 367
 DB 245 CAAGCGCAGCTCCGGGAGATCAAGCTCTTCAGGACCTTCGACGAGAGAAATCATAGG 304
 QY 368 CATCAGGATGTGATCCCGCGCGATCCCTCAGCGGTTCAACGAGCTCTACATGCCAC 427
 DB 305 CATCAGGAGATGTATCCCGCGCGATCCCGCGCGGTTCAACGAGCTCTACATGCCAC 364
 QY 428 GAGGCTCATGAGACACGAGCTTCATCATCATCATCTCCGCTCAACCAAGAACTGTCAAGAGA 487
 DB 365 GAGGCTCATGAGACACGAGCTTCATCATCATCATCTCCGCTCAACCAAGAACTGTCAAGAGA 384
 QY 488 GCACTGCCAGTATTTCTGTACAGATCTCTGGGGGGCTCAAGTACATCATCTCCACTCGCGGAA 547
 DB 385 ----- 384
 QY 548 CGTGATCCACCGGAGCTTGAAGCCGAGCAACCTGCTGTGAACCCCACTTCGACCTCAA 607
 DB 385 -----TCCACCGGAGCTTCAAGCCAGCAACCTGCTGTGAACCCCACTTCGACCTCAA 439
 QY 608 GATCTCGAGCTTCGGGCTGGCGCGCGCTGTCGAGAGAGGACATGATGAGGAGTACGT 667
 DB 440 GATCTCGAGCTTCGGGCTGGCGCGCGCTTCTCCGAGAGCGACATGATGAGGAGTACGT 499
 QY 668 GGTCAACCGGTGTACCGCGCGCGAGCTGCTCACTCCACCGAGTACTCCGCGCG 727
 DB 500 GGTGACACGGTGTACCGCGCGCGAGCTGCTCACTCCACCGAGTACTCCGCGCG 559
 QY 728 CATCGAGCTCTGCTCGGCTCGGCTGCATCTTTCATGAGAGCTCATCAACCGCGAGCGCTCTT 787
 DB 560 CATCGAGCTCTGCTCGGCTCGGCTGCATCTTTCATGAGAGCTCATCAACCGCGAGCGCTCTT 619
 QY 788 CCCCAGGAGGACCATATGACACAGATGCGCTTCATCCGAGGTGATCGGAGCGCGGAC 847
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 QY 848 GAGAGGAGCTGGGTTTCATAGGACGAGGAGCGGAGGAGTACATGAGGAGCGCTGCG 907
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 DB 800 CCTCATCGAGAGGATGCTCACTTCAACCGCTGCGAGAGGATCATAGTTCAGGAGCGCT 859

KEYWORDS
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE
1 (bases 1 to 718)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 140 row: A column: 09
Seq primer: T7 promoter Primer.

FEATURES
source
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/organism="Saccharum officinarum"
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/db_xref="taxon:4547"
/clone="SCQSB1140A09"
/lab_host="DH10B"
/clone_lib="SBI"
/notes="Organ: Stalk Bark from adult plants; Vector:
pSport1; Site 1: SalI; Site 2: NotI; An unidirectional
cDNA library generated from [stalk bark from adult
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CU-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 43.8%; Score 611.4; DB 6; Length 718;
Best Local Similarity 91.4%; Pred. No. 3.9e-132;
Matches 656; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
107 GCGGAGATGACGACGCGCGCGGTACCTGCTCTAGGACATCTTCGGGACAAAGTTCCA 166
1 GCGGAGCGGTGACGACGCGCGCGGTCTCTGCGAGTACAAACATCTTCGGCAACCTGTTCGA 60
167 GGTGAGCAACAGTACGACGCGCGCGGTATGCGCCATGCGCGCGCGCTACGGGATCGT 226
61 GATCAGCGCAAGTACGACGCGCGGTATGCGCCATGCGCGCGCGCGCTACGGGATCGT 120
227 CTGCTCGGTGATGAACTTTGAGACGAGGAGATGTTGGCGGATTAAGAAAGATGCCAACGC 286
121 CTGCTCGGTGATGAACTTTGAGACGAGAGATGTTGGCGCATCAAGAAGATGCCAACGC 180
287 GTTCAACACGATGAGCGCGCGCGCGGTATGCGCGCGCGGTATGCGCGCGCGCTCTAGGACCT 346
181 CTTTCGACCAACCATGAGCGCGCGCGCGGTATGCGCGCGCGGTATGCGCGCGCGCTCTAGGACCT 240
347 CGACACGAGAAACATCATAGGATCATAGGATGATGATCCGCGCGCGGTATGCGCGCGGT 406
241 CGACACGAGAAACATCATAGGATCATAGGATGATGATCCGCGCGCGGTATGCGCGCGGT 300
407 CAACGAGCTTACATCGCCACGAGCTCATAGGACACCGACCTTCATCATCATCATCGCTC 466
301 CAACGAGCTTACATCGCCACGAGCTCATAGGACACCGACCTTCATCATCATCATCGCTC 360
467 CAACGAGCTTACATCGCCACGAGCTCATAGGACACCGACCTTCATCATCATCATCGCTC 526

Db 361 CAACGAGAGCTCTCGGAGGACCTGCCAGTACTTCTGTACAGATCTCTTGGGGGCT 420
QY 527 CAAGTACATCCACTCGGGAACGTCATCCACGCGACCTTGAAGCGGAGCAACCTGCTGCT 586
Db 421 CAAGTACATCCACTCGGGAACGTCATCCACGCGACCTTGAAGCGGAGCAACCTGCTGCT 480
QY 587 GAACGCCAATCGGACCTCAAGATCTCGGCTTTCGGGCTGGCGGCGCGCTCTCGGAGAG 646
Db 481 GAACGCCAATCGGACCTCAAGATCTCGGCTTTCGGGCTGGCGGCGCGCTCTCGGAGAG 540
QY 647 GCACATGATGACGAGTACGTCGTCACCGGTCACCGGTCACCGGTCACCGGTCACCGGTC 706
Db 541 GCACATGATGACGAGTACGTCGTCACCGGTCACCGGTCACCGGTCACCGGTCACCGGTC 600
QY 707 CTCCACCGACTACTCTCGGCGCATCGAGCTCTGTCGCTCGGCTGCATCTTCATGAGCT 766
Db 601 CTNACCGACTACTCTNCGGCGCATCGAGCTCTGTCGCTCGGCTGCATCTTCATGAGCT 660
QY 767 CATCAACCGCGCGCGCTCTCTTCCCGGCGGAGGACACATGACGAGATGCCCTCAT 823
Db 661 CATCAACCGCGCGCGCTCTCTTCCCGGCGGAGGACACATGACGAGATGCCCTCAT 718

RESULT 10
CK077805
LOCUS
DEFINITION
81986raicen_10007.Y1 Oryza sativa cv. LYP9 booting whole plant cDNA
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
ACCESSION
VERSION CK077805.1 GI:58689118
KEYWORDS
SOURCE EST.
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 632)
AUTHORS
Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
Wu, S. and Liu, J.
TITLE
The Genomes of Oryza sativa: A History of Duplications
JOURNAL
PUBMED PLoS Biol. 3 (2), e38 (2005)
COMMENT
15685232
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 632
POLYA=No.
Location/Qualifiers
1..632
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="LYP9"
/db_xref="taxon:39946"
/tissue_type="whole plant"
/dev_stage="booting"
/clone_lib="Oryza sativa cv. LYP9 booting whole plant cDNA
library"

ORIGIN
Query Match 43.6%; Score 608; DB 7; Length 632;
Best Local Similarity 99.5%; Pred. No. 2.4e-131;
Matches 621; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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6  GTCAGATAAGTCTGTTAATTAGTTGGTCAATTGGCTGCTTGGCGGCGAGAGAGAGAG 65
Db  |||||
12  GTCAGATAAGTCTGTTAATTAGTTGGTCAATTGGCTGCTTGGCGGCGAGAGAA---GAG 68
Qy  |||||
66  GAGGAGATTAGGATGACGCGGCGCGGTGGCGAGTTCAGGCGGCGAGATGACGACGCGC 125
Db  |||||
69  GAGGAGATTAGGATGACGCGGCGCGGTGGCGAGTTCAGGCGGCGAGATGACGACGCGC 128
Qy  |||||
126  GGCCTGCTACCTGCTACGACATCTTCGGGAACAAGTTCGAGGTGACGAACAAGTACCA 185
Db  |||||
129  GGCCTGCTACCTGCTACGACATCTTCGGGAACAAGTTCGAGGTGACGAACAAGTACCA 188
Qy  |||||
186  CGGCCCATATGCGCATTCGCGCGCGCTACGAGATGCTGCTCCGTGATGAATTTT 245
Db  |||||
189  CGGCCCATATGCGCATTCGCGCGCGCTACGAGATGCTGCTCCGTGATGAATTTT 248
Qy  |||||
246  GAGACGAGGAGATGCTGCGGATTAAGAAGATCGCCAAACGCTTCAACAACGACATGG 305
Db  |||||
249  GAGACGAGGAGATGCTGCGGATTAAGAAGATCGCCAAACGCTTCAACAACGACATGG 308
Qy  |||||
306  GCCAAGCGCAGCTCCGCGGAGATCAAGCTCCTCAGGCACTTCGACCAACGAGAACATCA 365
Db  |||||
309  GCCAAGCGCAGCTCCGCGGAGATCAAGCTCCTCAGGCACTTCGACCAACGAGAACATCA 368
Qy  |||||
366  GGCATCAGGATGTGATCCGCGCGCGCTCCCTCAGGCGGTTCAAACGCTTACATCGCC 425
Db  |||||
369  GGCATCAGGATGTGATCCGCGCGCGCTCCCTCAGGCGGTTCAAACGCTTACATCGCC 428
Qy  |||||
426  ACGGACTATGACACCGACCTCCATCATCATCGCTCCGCTCCCAACCAAGAACGTGAC 485
Db  |||||
429  ACGGACTATGACACCGACCTCCATCATCATCGCTCCGCTCCCAACCAAGAACGTGAC 488
Qy  |||||
486  GAGCACTGCCAGTATTTCTGTACAGATCCTCGCGGGCTCAAGTACATCCACTCGGCG 545
Db  |||||
489  GAGCACTGCCAGTATTTCTGTACAGATCCTCGCGGGCTCAAGTACATCCACTCGGCG 548
Qy  |||||
546  AACGTATCACCAGGACCTGAAGCGGAGCACTGCTGTGTAACGCGCACTCGGACCTC 605
Db  |||||
549  AACGTATCACCAGGACCTGAAGCGGAGCACTGCTGTGTAACGCGCACTCGGACCTC 608
Qy  |||||
606  AAGATCTGCGACTTCGGCTGGCG 629
Db  |||||
609  AAGATCTGCGACTTCGGCTGGCG 632

RESULT 11
C99344
LOCUS
DEFINITION
C99344 Rice panicle at ripening stage Oryza sativa (japonica
cultivar-group) cDNA clone E10732_82, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 608)
REFERENCE
Sasaki,T.
Rice cDNA from panicle at ripening stage
Unpublished (1996)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7461
Fax: 81-298-38-7468
Email: tsasaki@nri.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'
POLYANo. Location/Qualifiers

1. 508
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E10732_82"
/dev_stage="ripening stage"
/clone_lib="Rice panicle at ripening stage"
/note="Organ: panicle; Rice cDNA from panicle at ripening
stage"

Query Match 43.4%; Score 606.4; DB 5; Length 608;
Best Local Similarity 99.8%; Pred. No. 5.6e-131;
Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 787 TCCCGGCGGAGGACACATGACGAGATCGGCTCATCACCGAGGTGATCGGACGCCGA 846
Db 1 TCCCGGCGGAGGACACATGACGAGATCGGCTCATCACCGAGGTGATCGGACGCCGA 60
Qy 847 CGGACGACGAGCTGGGGTTTCATCGGAACGAGGACGCGAGGAGTACATGAGGACCTGC 906
Db 61 CGGACGACGAGCTGGGGTTTCATCGGAACGAGGACGCGAGGAGTACATGAGGACCTGC 120
Qy 907 CGCAGTACCGCGCGCGGAGCTTCGCGAGCATGTTCCCGGGGTGACGCCCGCGCTCG 966
Db 121 CGCAGTACCGCGCGCGGAGCTTCGCGAGCATGTTCCCGGGGTGACGCCCGCGCTCG 180
Qy 967 ACTCATCGAGAGGATGCTCAGCTTCAACCCGCTGCAGAGAAATCACAGTTGAGGAGCGCG 1026
Db 181 ACTCATCGAGAGGATGCTCAGCTTCAACCCGCTGCAGAGAAATCACAGTTGAGGAGCGCG 240
Qy 1027 TCGATCATCTTACCTAGAGAGATTGACGACATCGCCCATGAGCCCATCTGCTGGAGC 1086
Db 241 TCGATCATCTTACCTAGAGAGATTGACGACATCGCCCATGAGCCCATCTGCTGGAGC 300
Qy 1087 CTTCTCTCTTCGACTTCGAGCAGAGGCTTAAACGAGGACCAAAATGAGACGCTGATCT 1146
Db 301 CTTCTCTCTTCGACTTCGAGCAGAGGCTTAAACGAGGACCAAAATGAGACGCTGATCT 360
Qy 1147 TCACGAAGCGGATCGAGATGAACCCCAACATCCGCTACTAGATTGAATCACCATGGAAT 1206
Db 361 TCACGAAGCGGATCGAGATGAACCCCAACATCCGCTACTAGATTGAATCACCATGGAAT 420
Qy 1207 GAGATCCCTCTATACCTCTTGTATATATGATGAAGATTGAGACCGGGTGAAGTAA 1266
Db 421 GAGATCCCTCTATACCTCTTGTATATATGATGAAGATTGAGACCGGGTGAAGTAA 480
Qy 1267 CATTGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1326
Db 481 CATTGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
Qy 1327 TTGTATGATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1386
Db 541 TTGTATGATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Qy 1387 AAAAAAAA 1394
Db 601 AAAAAAAA 608

RESULT 12
CF243446
LOCUS
DEFINITION
CF243446 3530 bp mRNA linear EST 06-AUG-2003
Invitrogen From multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
```


clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 819)

Walbot, V

Maize ESTs from various cDNA libraries sequenced at Stanford

MAIZE ESTB FROM VARI
University

University
Unpublished (1999)

Contact: Walbot V

Contact: Walbot V.
Department of Biological Sciences

Department of Biology
Stanford University

Stanford University
855 California Ave. Palo Alto, CA 94304. USA

Tel: 650 723 2227

TEL: 650 725 8221
FAX: 650 725 8221

Fax: 650 723 8221
Email: walbot@stanford.edu

Email: wardoc@scailord.edu
 Plate: 3530 1 21 1 row: C column: 01.

Trace: 0001211 LOW: C

1. .819

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1. .013
/organism="Zea mays"
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/mol type="mrna"

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/mot_type="ILKNA"
/cultivar="B73"
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/current= 673  
/db xref="taxon:4577"
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/w_xref=caxon:4377/
/tissue type="multiple"
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/dev stage="varies by tissue"
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/dev_stage= vardev  
/lab_host="DH10B"
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/clone_lib=3530 - Full length cDNA library created by
 Invitrogen from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
 Project contrasted with Invitrogen to produce a
 normalized, full length library in a pSPORT vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZmDB in the EST library description tables. poly(A)+
 mRNA was prepared by Invitrogen, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 dap aleurone; 4. Immature tassels, stages from
 1.2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
 12 dap endosperm and embryo; 12. 17 dap endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 Unigene clones from the Maize Gene Discovery EST
 sequencing projects. Clones can be ordered through the
 ZmDB web site or directly from the University of Arizona
 (<http://www.genome.arizona.edu/orders/>). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

ORIGIN

Query Match 43.3%; Score 603.8; DB 6; Length 819;
Best Local Similarity 98.7%; Pred. No. 2.4e-130;
Matches 653; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy	48	CGCGCAGAGAGAGGAGGAGGATTTAGGATGAGACGGGGCGCCCGGTGCGGAGTTTCAG	107
Db	84	GCCTCGAGGAGAGATGAGCGGAGGAGCGGTGGACGGAGCTCCGGTCGCCGAGTTCCGG	143
Qy	108	CCGACGATGACGACGCGCGCGGTACTGTCTTACGACATCTTTCGGGAAACAAGTTTCAG	167
Db	144	CAGACGGTGGACGACGCGCGCGGGTTCCTGCAGGTACAACATCTTCGGCMACTCTGTTTCAG	203
Qy	168	GTGACGAAACAAGTACCAAGCGCCGCCATCATGCCCCATTGGCCGCGGGCTTACGGGATCGTC	227

/tissue_type="roots"		/lab_host="XLOLR"		/clone_lib="Hordeum vulgare Barke roots"		/note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2: XhoI; mRNA was made from roots of spring barley variety 'Barke', a high quality malting variety. Roots were grown for two days on filter paper at room temperature. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artifact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb. Sequence trimming: vector sequences and sequence ends were trimmed from the 5'- and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"	
Query Match	42.7%	Score	595.4	DB 1	Length	700	
Best Local Similarity	91.4%	Pred.	No. 2.1e-128				
Matches	629	Conservative	0	Mismatches	59	Indels	0
Gaps	0						
Qy	219	GGGATCGTCTGCTCCGTTGATGAACCTTTTGAGACGAGGAGATGGTGGCGATAAAGAAGATC	278				
Db	13	GGNATCGTCTGCTCCGTTGATGAACCTTCGAGACGAGGAGATGGNGCAATCAAGAAGATC	72				
Qy	279	GCCAAACGGTTCAACAACGACATCGACGCCAAGCGCAGCTCCCGGAGATCAAGCTCCTC	338				
Db	73	GCAAAACGCTTCGACAAACAACATGGACGCCAAGCGCAGCTCCCGGAAATCAAACTCCTC	132				
Qy	339	AGGCACCTCGACACGAGAACATCATAGGCATCAGGGATGTGATCCCGCCGCCGATCCCT	398				
Db	133	AAGCACCTCGACACGAGAACATAGTAGGCCTTCGAGACGTGATCCCGCCGCCGATCCCG	192				
Qy	399	CAGCGGTTCAACGAGCTTACATCGCCACGGAGTCTATGACACCGACCTCCATCAATC	458				
Db	193	CAGTCTTCAACGAGCTTACATCGCCACTGAGTCTATGGACACGGACCTTCACCAATC	252				
Qy	459	ATCCGCTCCAAACGAAGAACTGTCAAGAGAGACACTGCCAGTATTTCTGTACCAAGATCTG	518				
Db	253	ATCCGTTCCAAACGAAGAACTCTCAAGAGAACACTGCCAGTACTTCTGTGTACAGTCTGT	312				
Qy	519	CGGGGGCTCAAGTACATCCACTCGCGCAACGTGTATCCACCGGACCTGGAAGCCGAGCAAC	578				
Db	313	CGCGGTCTCAAGTACATCCACTCGCGGAAACGTGTATCCATCGGACCTGGAAGCCGAGCAAC	372				
Qy	579	CTGCTGTGAACCGCAACTGCGAATCTGCGAATCTGGGCTTGGCGGCTGGCGCGGCGGTG	638				
Db	373	CTGCTGTGAACCGCAACTGCGAATCTGCGAATCTGGGCTTGGCGGCTGGCGCGGCGGTG	432				
Qy	639	TCGAGAGCGCATGATGACGAGTACGTGTGTCAACCGGTGATACCGCGCGCCGAGCTG	698				
Db	433	TCGAGAGCGCATGATGACGAGTACGTGTGTCAACCGGTGATACCGCGCGCCGAGCTG	492				
Qy	699	CTGCTCAACTCCACCGACTACTCGCGCGCCATCGACGCTCTGGTCCGTGCGGTGATCTTC	758				
Db	493	CTGCTCAACTCCACCGACTACTCGCGCGCCATCGACGCTCTGGTCCGTGCGGTGATCTTC	552				
Qy	759	ATGAGCTCATCAACCGCAGCGCTCTTCCCGCGGACGAGCACCATGCAACAGATGCGC	818				
Db	553	ATGAGCTCATCAACCGCAGCGCTCTTCCCGCGGACGAGCACCATGCAACAGATGCGC	612				
Qy	819	CTCATCACGAGGTGATCGGACGCGCGACGAGCACGAGCTGGGGTTTCATACGGAACGAG	878				
Db	613	CTCATCACGAGGTGATCGGACGCGCGACGAGCACGAGCTGGGGTTTCATACGGAACGAG	672				
Qy	879	GACCGGAGAAATCATGAGGCACTGCG	906				
Db	673	GACCGGAGAAATCATGAGGCACTGCG	700				

[illegible]

sativa cDNA clone S040D07, mRNA sequence.
BI805515
BI805515.1 GI:15852719
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 667)
Dong H.T., Li D.B., Zhuang X.F., Dai C.G., Sun L.X., Pei Y.X., Wu H.F., Jiang Y.X., Yu F.C., Gao Q.K. and Lou Y.C.
A Gene Expression Screen in *Oryza sativa*
Unpublished (2001)
Contact: Haitao Dong, Debao Li
Bioinformatics and Gene Network Research Group
Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: webmaster@estarray.org, URL: http://www.estarray.org
Seq primer: M13 forward primer.
Location/Qualifiers
1..667
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="S040D07"
/tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/clone_lib="Stem library from *Oryza sativa* (3-5 leaf stage)"
/notes="Vector: pSport2"

ORIGIN

Query Match 42.6%; Score 594.2; DB 3; Length 667;
Best Local Similarity 97.9%; Pred. No. 4.1e-128;
Matches 655; Conservative 0; Mismatches 8; Indels 6; Gaps 5;

QY 730 TCGACGTCGTGCGTCGGCT--GCATCTTCATGGAGCTCATCAACGGCCAGCGCGCTCTT 787
Db 1 TCGACGTCGTGCGTCGGCTTGCATGCTTCATGGAGCTCATCGACCGCA-CCGCTCTT 59

QY 788 CCCCGGAGGAGCCACATGCACAGATGCGCCTCATCACGAGGTGATCGGAGCGCGAC 847
Db 60 CCCC-GCAGGAGCCACATGCACAGATGCGCCTCATCACGAGGTGATC-GGAGCGCGAC 117

QY 848 GGCAGCAGCTGGGGTTCATACGGACAGGAGCGGAGGAAATPACATGAGGCACTTGCC 907
Db 118 GGCAGCAGCTGGGGTTCATACGGACAGGAGCGGAGGAAATPACATGAGGCACTTGCC 177

QY 908 GCAGTACCGCGCGGAGCGTTCGCGAGCATGTTCCGCGGGTGCAGCCCGCGCTCGA 967
Db 178 GCAGTACCGCGCGGAGCGTTCGCGAGCATGTTCCGCGGGTGCAGCCCGCGCTCGA 237

QY 968 CCTCATCGAGGATGCTCACCTTCAACCGCTGCAGAGATCACAGTTCAGAGGAGCGCT 1027
Db 238 CCTCATCGAGGATGCTCACCTTCAACCGCTGCAGAGATCACAGTTCAGAGGAGCGCT 297

QY 1028 CGATCATCTTACCTTAGAGAGATGTCACGACATCGCCGATGAGCCCAATCTGCTTGGAGCC 1087
Db 298 CGATCATCTTACCTTAGAGAGATGTCACGACATCGCCGATGAGCCCAATCTGCTTGGAGCC 357

QY 1088 CTCTCTCTCGACTTCGAGCAGAGGCTCTAAACGAGGACCAATGAGCAGCTGATCTT 1147
Db 358 CTCTCTCTCGACTTCGAGCAGAGGCTCTAAACGAGGACCAATGAGCAGCTGATCTT 417

QY 1148 CAACGAAGCGATCGAGATGAACCAACATCCCGTACTAGATTGAATCACCATGGAATG 1207
Db 418 CAACGAAGCGATCGAGATGAACCAACATCCCGTACTAGATTGAATCACCATGGAATG 477

QY 1208 AGATCCCGTCTATACCTGCTTTGTGACATATGATGATGAGAGCGGGTAGACTGAAC 1267

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2005, 02:45:39 ; Search time 617 Seconds
(without alignments)
15079.272 Million cell updates/sec

Title: US-10-768-886-1
Perfect score: 1396
Sequence: 1 agagagtcagataaggtcgt.....ttaaaaaaaaaaaaaaaaaa 1396

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1396	100.0	1396	13	Adt02329 Rice mito
2	920	65.9	1525	3	Aac44071 Zea mays
3	915.8	65.6	1125	4	Aac84259 Signal tr
4	808.4	57.9	1084	13	Adt02331 Rice mito
5	623.2	44.6	1837	13	Adt19687 Plant cdn
6	543	38.9	873	13	Ado84444 Plant ful
7	513	36.7	1197	4	Aac84265 Signal tr
8	511.2	36.6	1197	4	Aac84262 Signal tr
9	508.8	36.4	1188	3	Aac43105 Arabidops
10	508.8	36.4	1188	6	Abz12839 Arabidops
11	492.2	35.3	1637	13	Adx47615 Plant ful
12	485.8	34.8	1520	13	Adx53699 Plant ful
13	484.2	34.7	1546	3	Aac43674 Zea mays
14	484	34.7	1544	2	Aav27563 Salicylic
15	483.6	34.6	1119	4	Aac84253 Signal tr
16	483.2	34.6	1725	2	Aat60349 MAP kinas
17	467.8	33.5	1888	13	Adx11753 Plant ful
18	448.4	32.1	1786	2	Aat60350 MAP kinas
19	444	31.8	1718	6	Abn91076 Physcomit

20	427.8	30.6	629	11	ADM45543
21	425	30.4	1282	3	AAC33580
22	425	30.4	1359	3	AAC47261
23	399.6	28.6	1719	3	AAC48025
24	399	28.6	1451	3	AAC32826
25	398	28.5	1110	4	AAC84250
26	389.4	27.9	697	11	ADM44956
27	365.4	26.2	1116	3	AAC48312
28	354.2	25.4	1664	13	ADT20096
29	348.4	25.0	1122	3	AAC42749
30	339.6	24.3	1113	4	AAC84256
31	339.6	24.3	1654	3	AAC44676
32	338.8	24.3	1813	13	ACF87406
33	338.8	24.3	1837	14	ADM12904
34	338.8	24.3	1868	4	AAI59696
35	338.8	24.3	1869	4	AAI57910
36	337.2	24.2	1071	2	ABA96212
37	337.2	24.2	1140	10	ADH59631
38	337.2	24.2	1866	2	AAV62478
39	337.2	24.2	1866	6	ABK84604
40	337.2	24.2	1866	8	ACA89915
41	337.2	24.2	1866	12	ADO24424
42	337.2	24.2	1866	14	ADZ10042
43	337.2	24.2	1896	2	AAV71022
44	337.2	24.2	1896	3	AAD00036
45	337.2	24.2	3732	6	ABK90802

ALIGNMENTS

RESULT 1

ADT02329
ID ADT02329 standard; cdna; 1396 BP.

AC ADT02329;

DT 13-JAN-2005 (first entry)

DE Rice mitogen-activated protein kinase 5a (MAPK5a) cdna.

KW Rice; mitogen-activated protein kinase 5a; MAPK5; MAPK5a; gene; ss;
KW abiotic stress tolerance; biotic stress tolerance; drought; temperature;
KW salinity; plant.

OS Oryza sativa.

PH Key Location/Qualifiers

FT CDS 78..1187

FT /*tag= a

FT /product= "Rice MAPK5a"

FT /transl_except= (pos:729..734, aa:Asp)

XX US2004209325-A1.

XX 21-OCT-2004.

XX 31-JAN-2004; 2004US-00768886.

XX 31-JAN-2003; 2003US-0444249P.

XX (YANG/) YANG Y.

XX (XIONG/) XIONG L.

XX Yang Y, Xiong L;

XX WPI; 2004-747214/73.

XX P-PSDB; ADT02330.

XX GENBANK; AF479883.

XX New isolated nucleic acid molecule encoding a mitogen-activated protein
kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic
and biotic stress in plants.

PR 25-FEB-1999; 99US-0121925P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134376P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135553P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 16-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-014930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.

PR 14-MAY-1999; 99US-0134292P.
 PR 08-JUL-1999; 99US-0142996P.
 XX (PION-) PIONEER HI-BRED INT INC.
 PA Helentjaris TG;
 XX
 XX
 XX WPI; 2001-031929/04.
 DR P-PSDB; AAB48046.
 XX
 XX New signal transduction nucleic acids and encoded proteins useful for
 PT regulating phytohormone expression, including ethylene, auxins,
 PT cytokinins and gibberellin, to provide control of plant response to
 PT environmental stresses.
 XX
 XX Claim 1; Page 89-90; 126pp; English.
 XX
 XX The invention provides Zea mays signal transduction proteins and encoding
 CC nucleotide sequences. The nucleic acids are useful for regulating
 CC expression of phytohormones, including ethylene, auxins, cytokinins, and
 CC gibberellin, to effect developmental changes in plants and provide
 CC control of plant response to environmental stresses. They may also be
 CC used as probes or amplification primers in the detection, quantitation or
 CC isolation of gene transcripts, for detecting mutations in the gene, for
 CC monitoring upregulation of expression or changes in enzyme activity in
 CC screening assays of compounds, for detection of any number of allelic
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
 CC further be used for recombinant expression of their encoded polypeptides,
 CC as immunogens in the preparation or screening of antibodies, and in sense
 CC or antisense suppression of genes in a host cell, tissue or plant. The
 CC proteins may be used in assays for enzyme agonists or antagonists, as
 CC immunogens or antigens to obtain antibodies specifically immunoreactive
 CC with the proteins. The present sequence represents a cDNA encoding a
 CC signal transduction protein of the invention
 XX
 SQ Sequence 1125 BP; 241 A; 390 C; 317 G; 177 T; 0 U; 0 Other;
 Query Match 65.6%; Score 915.8; DB 4; Length 1125;
 Best Local Similarity 88.7%; Pred. No. 1.3e-178;
 Matches 992; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
 QY 69 GGATTAGGATGACGGGGCGCGGTGGCGGAGTTTCAGGCGCGATGACGACGGCGG 128
 DB 7 GGAGGAGCGTGACGCGAGCTCCGGTCCGCGAGTTCCGGCAGACGGTGACGACGGCGG 66
 QY 129 CGGTACCTGCTTACGACATCTTCGGGAACAAGTTTCAGGTGACGAAACAAGTACCAAGCCG 188
 DB 67 CGGTCTCTGAGTACACATCTTCGGCACTCTGTCGAGATCAGGCAACAGTACCAAGCC 126
 QY 189 CCCATCATGCCCATTGGCGCGCGGCTTACGGGATCGTCTGCTCCGTGATGAATTTGAG 248
 DB 127 CCCATCATGCCCATTGGCGCGCGGCTTACGGGATCGTCTGCTCCGTGATGAATTTGAG 186
 QY 249 ACAGGAGAGATGGTGGGATTAAGAAGTCCCAAGCGGTTCAACACGACATGAGCGCC 308
 DB 187 ACAGGAGAGATGGTGGGATTAAGAAGTCCCAAGCGGTTTCGCAACCAACATGAGCGCC 246
 QY 309 AAGCGCACGCTCCGGGAGATCAAGCTCTCAGGCACCTCCGACCAACGAGAACATCATAGGC 368
 DB 247 AAGCGCACGCTCCGGGAGATCAAGCTCTGAGGCACCTCCGACCAACGAGAACATCATAGGC 306
 QY 369 ATCAGGAGATGATGATCCCGCGCGGATCCCTCAGCGGTTCAACGACGCTTACATCCGACG 428
 DB 307 ATCAGGAGATGATGATCCCGCGCGGATCCCTCAGCGGTTCAACGACGCTTACATCCGACG 366
 QY 429 GAGCTCATGACACGACCTCCATCATCATTCGCTCCACCAACGAGACTGTCAGAGAG 488
 DB 367 GAGCTCATGACACGACCTCCATCATCATTCGCTCCACCAACGAGACTGTCAGAGAG 426
 QY 489 CACTGCGAGATATTTCTGTACAGATCTTCGGGGGGCTCAAGTATACATCCATCCGCGGAAC 548
 DB 427 CACTCCCAAGTACTTCAATGATACAGATCTTCGGGGGGCTCAAGTATACATCCATCCGCGGAAC 486

QY 549 GTGATCCACCGGACCTGAAGCGGAGCAACCTGCTGTAAGCGCAACCTGCGACCTCAAG 608
 DB 487 GTGATCCACCGGACCTGAAGCGGAGCAACCTGCTGTAAGCGCAACCTGCGACCTCAAG 546
 QY 609 ATCTGCGACTTCGGGCTGGCGGGCGGTGTCGGGAGCGACATGATGACGAGTACGTG 668
 DB 547 ATCTGCGACTTCGGGCTGGCGGGCGGTGTCGGGAGCGACATGATGACGAGTACGTG 606
 QY 669 GTACCCCGGTGTACCGCGCGGCGGAGCTGCTCAACTCCACCGACTACTCCGCGGCC 728
 DB 607 GTACCGCGTGTGTACCGCGCGGCGGAGCTGCTCAACTCCACCGACTACTCCGCGGCC 666
 QY 729 ATCGAGCTGTGCTCGGTGGCTGCACTTTCATGAGAGCTCATCAACCGCGAGCGCTCTTC 788
 DB 667 ATCGAGCTGTGCTCGGTGGCTGCACTTTCATGAGAGCTCATCAACCGCGAGCGCTCTTC 726
 QY 789 CCCGGCAGGACACATGACACGAGATGCGCTCATCACCGAGGTGATCGGAGCGCGACG 848
 DB 727 CCCGGCAGGACACATGACACGAGATGCGCTCATCAACCGAGGTGATCGGAGCGCGACG 786
 QY 849 GACGAGAGCTGGGTTTCATGCGAAGAGGAGCGGAGGAGTACATGAGGACCTGCGCG 908
 DB 787 GACGATGAGCTGGGTTTCATGCGAAGAGGAGCGGCGGAGTACATGCGGACCTGCGCG 846
 QY 909 CAGTACCCCGCGGAGCTTCGCGAGCATGTTCCCGCGGTCGAGCCCGCGGCTCGAC 968
 DB 847 CAGTTCGCCCGCGGCGGTTCGTCAGCTGTTCCCGGAGTACGCGGCTGCGCTGGAC 906
 QY 969 CTCATCGAGAGATGCTCACTTTCAACCGCTGCGAGAGTACACAGTTCAGGAGGCGCTC 1028
 DB 907 CTCATCGAGAGATGCTCACTTTCAACCGCTGCGAGAGTACACAGTTCAGGAGGCGCTC 966
 QY 1029 GATCATCTTACCTAGAGAGATGACAGCATCGCGGATGAGCCCATCTGCTGAGAGCCC 1088
 DB 967 GAGCACCCGTACCTGGAAGCGGTACACGAGCTGCGCGAGCGAGCCCATCTGACAGGACCCG 1026
 QY 1089 TTCTCTCTGACTTCGAGCAGAGAGGCTCTAAACGAGGAGCCAAATGAAGCAGCTGATCTTC 1148
 DB 1027 TTCTCTCTGACTTCGAGCAGAGAGGCTCTGAGCGAGAGGCTCTGAGCGAAGACCAATGAAGCAGCTGATCTTC 1086
 QY 1149 AACGAGAGCATCGAGATGAACCCCAACATCCCGTACTAG 1187
 DB 1087 AACGAGAGCATCGAGATGAACCCCAACATCCCGTACTAG 1125
 RESULT 4
 ADT02331
 ID ADT02331 standard; cDNA; 1084 BP.
 XX
 AC ADT02331;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Rice mitogen-activated protein kinase 5b (MAPK5b) cDNA.
 XX
 XX Rice; mitogen-activated protein kinase 5b; MAPK5; MAPK5b; gene; ss;
 KW abiotic stress tolerance; biotic stress tolerance; drought; temperature;
 KW salinity; plant.
 XX
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 CDS 78..875
 FT /*tag= a
 FT /product= "Rice MAPK5b"
 FT /transl_except= (pos:1..6, aa:Met-Met-Asp)
 XX
 PN US2004209325-A1.
 XX
 PD 21-OCT-2004.
 XX
 PP 31-JAN-2004; 2004US-0076886.
 XX

PR 31-JAN-2003; 2003US-0444249P.
XX (YANG/) YANG Y.
PA (XIONG/) XIONG L.
XX Yang Y, Xiong L;
PI WPI; 2004-747214/73.
XX P-PSDB; ADT02332.
DR GENBANK; AF479884.
XX
PT New isolated nucleic acid molecule encoding a mitogen-activated protein
PT Kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic
PT and biotic stresses in plants.
XX
PS Claim 11; SEQ ID NO 3; 36pp; English.
XX
CC The invention relates to a rice mitogen-activated protein kinase 5
CC (MAPK5) polypeptides and the polynucleotides encoding them. The invention
CC also relates to an antibody that specifically binds to a peptide
CC consisting of a C-terminal portion of a MAPK5 polypeptide, a transgenic
CC plant transformed by a polynucleotide encoding a MAPK5 orthologue where
CC over expression of the MAPK5 orthologue in the plant results in increased
CC tolerance to abiotic stress compared to a wild-type plant and a method
CC for evaluating a plant for tolerance to abiotic stress comprising
CC treating a plant with abiotic stress, isolating a MAPK5 protein from the
CC plant, detecting MAPK5 activity and evaluating the increase or decrease
CC in MAPK5 activity in the plant where the increase in MAPK5 activity
CC indicates the plant is tolerant to abiotic stress. The methods and
CC compositions of the present invention are useful for increasing tolerance
CC to abiotic and biotic stress in plants using MAPK5, where the abiotic
CC stress is drought, temperature or salinity and the biotic stress is from
CC pathogenic bacteria, viruses, nematodes and insects. This sequence
CC represents cDNA encoding the rice MAPK5b polypeptide of the invention.
XX
SQ Sequence 1084 BP; 262 A; 288 C; 316 G; 218 T; 0 U; 0 Other;

Query Match 57.9%; Score 808.4; DB 13; Length 1084;
Best Local Similarity 99.9%; Pred. No. 1.5e-156;
Matches 809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 587 GAACGCCAAGTGGAGCTCAAGATCTCGACTTCGGGCTGGCGCGCGCTCGTCGAGAG 846
DB 275 GATCGCCAACTGGAGCTCAAGATCTCGACTTCGGGCTGGCGCGCGCTCGTCGAGAG 334
QY 647 CGACATGATGACGGAGTACGTGTGTACCCGGTGGTACCGCGCGCGAGCTGTCTCAA 706
DB 335 CGACATGATGACGGAGTACGTGTGTACCCGGTGGTACCGCGCGCGAGCTGTCTCAA 394
QY 707 CTCACCGACTACTCCGCGCCATCGACGCTGTGGTCCGTCGGTGTGATCTTCATGAGCT 766
DB 395 CTCACCGACTACTCCGCGCCATCGACGCTGTGGTCCGTCGGTGTGATCTTCATGAGCT 454
QY 767 CATCAACCGCAGCGCTCTTCCCGCGGAGGACCATGACCATGCGGCTCATCAC 826
DB 455 CATCAACCGCAGCGCTCTTCCCGCGGAGGACCATGACCATGCGGCTCATCAC 514
QY 827 CGAGGTGATCGGAGCGCGGACGACGAGCTGGGGTTTCATACGGAACGAGGACCGAG 886
DB 515 CGAGGTGATCGGAGCGCGGACGACGAGCTGGGGTTTCATACGGAACGAGGACCGAG 574
QY 887 GAAGTACATGAGGACCTGCGCAGTACCCCGCGCGAGAGCTTCGCGAGCATGTTCCCGCG 946
DB 575 GAAGTACATGAGGACCTGCGCAGTACCCCGCGCGAGAGCTTCGCGAGCATGTTCCCGCG 634
QY 947 GGTGACCGCGCGCGCTCGACCTCATCGAGAGATGCTCACCTTCAACCGCTCGAG 1006
DB 635 GGTGACCGCGCGCGCTCGACCTCATCGAGAGATGCTCACCTTCAACCGCTCGAGAG 694
QY 1007 AATCACAGTTGAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGACGACATCGCCGA 1066
DB 695 AATCACAGTTGAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGACGACATCGCCGA 754

QY 1067 TGAGCCCATCTGCTCGAGCCCTTCTCTTCTGACTTCGAGCGAAGGCTCTAAACGAGA 1126
DB 755 TGAGCCCATCTGCTCGAGCCCTTCTCTTCTGACTTCGAGCGAAGGCTCTAAACGAGA 814
QY 1127 CCAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCCGGTACTA 1186
DB 815 CCAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCCGGTACTA 874
QY 1187 GATTGAATCACCATGGAATGAGATCCCGTCTATACCTGCTTTGTACATATATGATCAAGAT 1246
DB 875 GATTGAATCACCATGGAATGAGATCCCGTCTATACCTGCTTTGTACATATATGATCAAGAT 934
QY 1247 TGAGAGCCGGTAGACTGAACATTCGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1306
DB 935 TGAGAGCCGGTAGACTGAACATTCGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 994
QY 1307 CTCTCAAGTTGTGGCTGCTTTGTATGATATATATGATGTTCTGATATGTTGTTGTTGTTG 1366
DB 995 CTCTCAAGTTGTGGCTGCTTTGTATGATATATATGTTGTTGTTGTTGTTGTTGTTGTTG 1054
QY 1367 GAACCTTTGGATTAAAAAATAAAAAA 1396
DB 1055 GAACCTTTGGATTAAAAAATAAAAAA 1084

RESULT 5
ADT19687
ID ADT19687 standard; cDNA; 1837 BP.
XX AC ADT19687;
XX DT 13-JAN-2005 (first entry)
XX DE Plant cDNA, Seq ID 5013.
XX KW Plant; ss; gene; transgenic; cold tolerance; growth rate;
KW drought tolerance; disease resistance; galactomanan production;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW lignin production; extreme osmotic condition tolerance;
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;
KW seed protein yield.
XX OS Viridiplantae.
XX PN US2004216190-A1.
XX PD 28-OCT-2004.
XX PF 18-DEC-2003; 2003US-00739930.
XX PR 28-APR-2003; 2003US-00424599.
XX PR 28-APR-2003; 2003US-00425115.
XX PA (KOVA/) KOVALIC D K.
XX PI Kovalic DK;
XX WPI; 2004-757369/74.
XX PT New recombinant DNA constructs useful in the field of biochemistry and
PT Genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.
XX PS Claim 1; SEQ ID NO 5013; 14pp; English.
XX CC The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region

functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

Sequence 1837 BP; 393 A; 594 C; 477 G; 373 T; 0 U; 0 Other;

Query Match 44.6%; Score 623.2; DB 13; Length 1837;

Best Local Similarity 70.9%; Pred. No. 2.1e-118;

Matches 892; Conservative 0; Mismatches 343; Indels 23; Gaps 4;

QY	53	GAGAGAGAGGAGGAGGATAGGATGGACGGGGCGCGCGGAGTTCCAGGCGGAC	112
DB	373	GAGAGTTTCGTGGCGCGTGTGAGATGGACGGCGCTCGGGTGGCGGCGGAC	432
QY	113	GATGACGACGGCGCGCGTCTCTACGACATCTTCGGGAAACAAGTTCCAGAGTGAC	172
DB	433	GATGACGACGCGCGCGCTCTCTCTACACATATTCGGCAACAGTTCCAGATCAC	492
QY	173	GAAACAAGTACAGCGCGCCATATGCCCCATTGGCGCGCGCTACGGGATGCTGCTC	232
DB	493	GGCCAAAGTACAGCGCGCGATCATGCCATCGCGCGCGCGCTACGGGATGCTGCTC	552
QY	233	CGTGATGAACTTTGAGACGGAGGAGATGGTGGCATAAAGATGCCAACGGTTCAA	292
DB	553	GGTGATGAACTTCGAGACGGAGGAGATGGTGGCAATCAAGATGCCAACGTTTCCA	612
QY	293	CAACGACATCGACGCCAAGCGCAGCTCCGGGAGATCAAGCTCTCAGGCACCTCGACCA	352
DB	613	CAACACATGACGCCAAGCGCAGCTCCGGGAGATCAAGCTCTGAGGCACCTCGACCA	672
QY	353	CGAGAACATCATAGGCATCAAGGATGTGATCCCGCGCGCGATCCCTCAGCGGTTCAACGA	412
DB	673	CGAGAACATAGTAGGCTTCGAGATGTGATCCCGCGCGCGACCGCGAGTCTTCAACGA	732
QY	413	CGTCTACATCGCACGGAGCTCATGGACACGGACCTTCATCATATCCGCTCCACCA	472
DB	733	CGTCTACATCGCACCGAGCTCATGGACACGGACCTTCATCATATCCGCTCCCGCA	792
QY	473	AGAACTGTCAAGAGACACTGCCAGTATTTCTGTACAGATCTCTGGGGGGGTCTCAAGTA	532
DB	793	AGCGCTCTCGAGAGAACACTGCCAGTATTTCTGTGGGGCGCGGGAGCGCGAGCA	852
QY	533	CATCCACTCGCGCGAACCTGTATCCACCGGACCTTGAAGCGGACCACTGTGCTGAACGC	592
DB	853	CATCTCACGGCACTCGTGGCGCGCCACCGAGGTCTGGTCCGCGAGCTGCATCTTTCATGC	912
QY	593	CAACTCGGACCTCAAGATCTGCGGACTTCGGGCTGGCGCGCGCTGTCGGAGAGCGACAT	652

DB	913	CGCCCATCAACCGCGGTCTCTCCCGGGAGGAGCACCATGCACAGATGCCGCTAT	972
QY	653	GATGACGGAGTACGTGGTCAACCGGTGTGATACCGCGC-----GCCGGAGCTGCTGC	702
DB	973	GCACGGGGGTGATCTGTCAACCCCGCCGACAGACGACCCCGATTCACCCGGACCGAGGAC	1032
QY	703	TCAACTCCACCGACTACTTCGGCGGCATCGACGTCTGGTCCGTCCGGCTGCATCTTCATGG	762
DB	1033	GCAGAGGATACATGAGGCACCTGCGCGGATTCCTTCGCGGCTCTTCCAGGGCCAGTT	1092
QY	763	AGCTCATCAACCGCCAGCGCTCTTCCCGGCA--GGGACCAATGCACACAGATGGCGCT	820
DB	1093	CCCCAAGGTGCAGCGCGCGCTGGCACCTCATCGAGAGGATATTCACCTGATACGGCT	1152
QY	821	CATCACCGAGGTGATCGGACCGCGGACGACGAGCTGGGGTTTATACGGAACAGGA	880
DB	1153	TATCACGGATGTATCGGACCCCGACCGACGACCTGGGTATTAATCCGGAACAGGA	1212
QY	881	CGCGAGGAGTACATGAGG--CACCTGCCGCGAGTACCGCGCGGAGCTTCCGCGACATGT	939
DB	1213	CGCCAGGAGTACATGAGGCGCACCTGCGCGAGTTCCTTCGCGGCTCTTCCCGGACAGT	1272
QY	940	TCCCGCGGTGCAGCGCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCCGC	999
DB	1273	TCCCGAAGGTGCAGCGCGCGCGCTGGAATCATCGAGAGGATGCTCACCTTCAACCCCGC	1332
QY	1000	TGCAGAGATCAAGTTGAGGAGGCGCTCGATCATCTTACCTAGAGAGATTCGACGACA	1059
DB	1333	TGCAGAGGATCAAGTTGAAGAGGCGCTGAGCACCATACCTAGAGCGGCTTTCAGACG	1392
QY	1060	TGCGCATGAGCCCATCTGCTGGAGCCCTTCTCTCGACTTCGAGCAGAGGCTCTAA	1119
DB	1393	TGCGCAGCAGGCGCATCTGCACGAGCCCTTCTCTTCGACTTCGAGCAGCAGCCACTGA	1452
QY	1120	ACGAGACCAAAATGAAGCAGCTGATCTTCAACGAGCGATCGAGATGAACCCCAACATCC	1179
DB	1453	CGGAGACCATGAGAGAGCTCATATTCAACGAGCCCTGGAGTTGAGCCCACTTCC	1512
QY	1180	GGTACTAGA-----TTGAATCACCATGGAAATGAGATCCCTCTATACCTGCTTT	1229
DB	1513	GATACTAGACGATTCTTCTAGTACCCCAATAGTATGATTTGATGTAAACTGTGTTG	1572
QY	1230	GTACATATGATCAGATTGAGAGCGCGGTAGACTGAACATTGCAATTTGTTGTTGTT	1287
DB	1573	TAATAGGATAGGTCAAGAGACATGGTAGATTGCGCACATGCAATTTGTTGTTGTT	1630

RESULT 6

AD084444

ID AD084444 standard; cDNA; 873 BP.

XX

AC AD084444;

XX

DT 21-APR-2005 (first entry)

XX

DE Plant full length insert polynucleotide seqid 3164.

XX

KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.

OS Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX

28-APR-2003; 2003US-00425114.
06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
(LIUJ/) LIU J.
(ZHOU/) ZHOU Y.
(KOVA/) KOVALIC D K.
(SCRE/) SCREEN S E.
(TABA/) TABASKA J B.
(CAOY/) CAO Y.
Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y;
WPI; 2004-180133/17.
New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
Claim 1; SEQ ID NO 3164; 15pp; English.
The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.
Sequence 873 BP; 181 A; 277 C; 237 G; 178 T; 0 U; 0 Other;
Query Match 38.9%; Score 543; DB 13; Length 873;
Best Local Similarity 89.3%; Pred. No. 5.8e-102;
Matches 585; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 537 CACTCGGCGAACGTGATCCACCGGACCTGAAGCCGAGCAACCTGCTGTGAACGCCAAC 596
DB 1 CACTCGGCGAACGTGATCCACCGGACCTGAAGCCGAGCAACCTGCTGTGAAGGCCAAC 60
QY 597 TGGACCTCAAGATCTCGGACTTCGGGCTGGCGGCGGCGGCTGTCGAGAGCGCATGATG 656
DB 61 TGGACCTCAAGATCTCGGACTTCGGGCTGGCGGCGGCGGCTGTCGAGAGCGCATGATG 120
QY 657 ACGGAGTACGTGTGTACCGGCTGGTACCGGCGGCGGAGTGTGTCTCAACTCCACCGAC 716
DB 121 ACGGAGTACGTGTGTACCGGCTGGTACCGGCGGCGGAGTGTGTCTCAACTCCACCGAC 180
QY 717 TACTCCGCGCCCATCGACGTCTGGTCCGTGGGCTGTCATGAGGCTCATCAACCGC 776
DB 181 TACTCCGCGCCCATCGACGTCTGGTCCGTGGGCTGTCATGAGGCTCATCAACCGC 240
QY 777 CAGCGGTCTTCCCGCGGAGGACCATGACACAGATGGCGCTCATCCAGGAGTGATC 836
DB 241 CAGCGGTCTTCCCGCGGAGGACCATGACACAGATGGCGCTCATCAACCGGAGTGATC 300
QY 837 GGCAGCCGACGACGACGAGCTGGGTTTCATACGGAACGAGGACCGAGGAGTACATG 896
DB 301 GGCAGCCGACGACGAGTGTGAGTCTGGGTTTCATCCGGAACGAGGACCGGAGGAGTACATG 360
QY 897 AGGCACCTGCGCGCAGTACCGCGCGGACGTTTCGCGAGCATGTTTCCCGCGGCTGACGCC 956

DB 361 CGCCACCTCCGCGAGTTCCGCGCGCGCGGCTTTCGTCAGCCTGTTCCCGGATGAGGCC 420
QY 957 GCGCGCTCGACCTCATCGAGGAGTGTCAACCTTCAACCGCTCGAGAGATCACAGTT 1016
DB 421 GTCGCGCTGAGACCTCATCGAGGATGTCACTTCAACCGCTCGAGAGATCACAGTG 480
QY 1017 GAGGAGGCGCTCGATCATCTTACCTAGAGAGATTGCACGACATCCCGGATGAGCCCATC 1076
DB 481 GAAAGAGCGCTGGAGCACCGGTACCTGGAAACGGCTACACGAGCTGCGCGAGGCCATC 540
QY 1077 TGCCTGAGGCGCTTCTCTTCTGACCTTCGAGAGAGAGGCTCTAAACGAGGACCAATGAG 1136
DB 541 TGCACGAGCGCGGTTCTCTGTTGACTTCGAGCAGCAGGCTCTGACGGAAGACCAATGAG 600
QY 1137 CAGCTGTGATCTCAACGAGCGATCGAGATGAACCCAAACATCCCGTACTAGATTG 1191
DB 601 CAGCTGTGATCTCAACGAGCGCATCGAATCAACCCAACTTCGGATACTAGCTAG 655
RESULT 7
AAC84265
ID AAC84265 standard; cDNA; 1197 BP.
XX
AC AAC84265;
XX
DT 19-MAR-2001 (first entry)
XX
DE Signal transduction protein encoding cDNA.
XX
KW Zea mays; maize; signal transduction protein; phytohormone; ethylene;
KW auxin; cytokinin; gibberellin; immunogen; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
CDS 1..1197
FT /*tag= a
FT /product= "signal transduction protein"
XX
PN WO200070059-A2.
XX
PD 23-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011687.
XX
PR 14-MAY-1999; 99US-0134292P.
PR 08-JUL-1999; 99US-0142996P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Helentjaris TG;
XX
XX WPI; 2001-031929/04.
DR P-PSDB; AAB48048.
XX
PT New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses.
XX
PS Claim 1; Page 95-96; 126pp; English.
XX
CC The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins, and
CC gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may

CC further be used for recombinant expression of their encoded polypeptides,
 CC as immunogens in the preparation or screening of antibodies, and in sense
 CC or antisense suppression of genes in a host cell, tissue or plant. The
 CC proteins may be used in assays for enzyme agonists or antagonists, as
 CC immunogens or antigens to obtain antibodies specifically immunoreactive
 CC with the proteins. The present sequence represents a cDNA encoding a
 CC signal transduction protein of the invention

XX Sequence 1197 BP; 317 A; 306 C; 281 G; 293 T; 0 U; 0 Other;

Query Match 36.7%; Score 513; DB 4; Length 1197;
 Best Local Similarity 67.4%; Pred. No. 9.2e-36;
 Matches 739; Conservative 0; Mismatches 355; Indels 3; Gaps 1;

QY	87	GC	CGCGGTGCGGAGTTTCAGCGCGAGTACGACGCGCGCGCGCGTACCTGCTCTACGAC	146
DB	103	GG	GATGATGAGAACATCCACGCGACGCTCAGCCACGCGTGGCGCTTCATCCAGTACAC	162
QY	147	AT	CTTCGGGAACTTCGAGGTGACGAACAAGTACAGCGCGCCCATCATGCCCATTTGGC	206
DB	163	AT	CTTCGGGAACTTCGAGGTGACCTCCAGTACAAAGCCCGCCCATCTCCCGATCGGC	222
QY	207	CG	CGCGCGCTACGCGGATCGTCTGCTCGTGATGAATTTTGAGACGAGGAGATGTTGGCG	266
DB	223	AAG	GCGCTACGCGATCGTCTGCTCGCGCTCACTCCGAGCGCGAGCGAGTGGCC	282
QY	267	ATA	AGAGATCGCCAAACGGTTTCAACACGACATGGAACGCCAAGCGCACGCTCCCGGAG	326
DB	283	AT	CAAGATGCGCAACGCTTCGACACCAAGATGATGATGCAAGCGCACGCTCCCGGAG	342
QY	327	AT	CAGCTCTCAGGACCTCGACCGACGACGACGACGACGACGACGACGACGACGACGAC	386
DB	343	AT	CAGCTGCTCGCGCCACATGGACCGACGACGACGACGACGACGACGACGACGACGAC	402
QY	387	CC	CGCGGATCCTCAGGCGTTCAACGCGTCTACATCCGCGGAGCTCATGGACACCGAC	446
DB	403	CT	CTCATTGAGGAGGATTCATGATGATGATGATGATGATGATGATGATGATGATGAT	462
QY	447	CT	CCATCATCATCTCGCTCAACCAAGAACTGTTCAGAGAGCACTGCCAGTATTTCCGT	506
DB	463	CT	GATCAAAATTTTCGTTCAATCAAGCTTTGTTCAGAGGAGCACTGTCAAGTATTTTCT	522
QY	507	TAC	CAGATCTCGCGGCGCTCAAGTATCATCCACTCGCGGAGCGTGTACCGCGGACCTG	566
DB	523	TAT	CAAAATTTCTCGTGGCTTGAAGTATATATATATATATATATATATATATATATAT	582
QY	567	AAG	CGGAGCAACTGCTGCTGAAACGCACTCGGACCTCAAGATCTCGGACTTCGGGCTG	626
DB	583	AAG	CTAGCAATCTTTTGAATGCAACTGTGACCTCAAGATATGATGATTTTGGGCTT	642
QY	627	GC	CGCGCGCTGCTCGGAGCGACATGATGACGAGTACGTTGCTCACCGGTGGTACCGC	686
DB	643	GCT	CGCACCACTCAGAAATGATTTTATGACTGAATATGTTGTCAAGATGATATAGA	702
QY	687	GC	CGCGGAGCTGCTGCTCACTCAACGACTACTCCGCGGATCGAGCTGTGCTCGTC	746
DB	703	GC	ACAGAGCTTTTATTTGAATCTCTGAAATATATATCTGCTGCAATGATGTTGCTGTG	762
QY	747	GG	CTGATCTTCATGGAGCTCATCAACCGCGCGCTCTTCCCGCGGAGGACACATG	806
DB	763	GG	CTGATATTTATGGAATGATGAGCGGAAACCTTTGTTCTGGAAGATCATGTC	822
QY	807	CAC	CAGATGCGCTCATCACCGAGTGTATCGGAGCGCGGAGCGGAGCTGGGGTTC	866
DB	823	CAT	CAGCTACGCTACTTAATGGAGCTCTTGGAAACCGAATAGGCTGATCTTGAATTT	882
QY	867	AT	ACGAGAGGAGCGGAGGAAATACATGAGGACCTTCGCGGATACCGCGCGGAGC	926
DB	883	GTA	---AATGAAATGCAAGAAGATATATTCGCCAACTTCCTGCTCATGCTAGACAGTCC	939
QY	927	TT	CGGAGCATGTTTCCGCGGGTGCAGCGCGCGCTTCGACCTCATCGAGAGATGCTC	986
DB	940	TT	CCCTGAAATTTTCCATGATGACACCTTTAGCAATTTGACCTAGTGGAAAGATGCTA	999

QY	987	AC	TTCAACCCGCTGCGAGAGATCACAGTTGAGGAGCGCTCGATCATCTTACCTAGAG	1046
DB	1000	AC	TTTGTATCTTAGACAGAGATAACTGTGTAAGGCGCACTTGACACACCTTACTTGGCA	1059
QY	1047	AG	ATTGCGAGCATCGCCCATGAGCCCATCTGCTGGAGCGCTTCTCTTCGACTTCGAG	1106
DB	1060	TC	ACTTCATGACATAAGTGTGATGAGCGAGTCTGCTCAATGCCCTTCAGCTTCGACTTCGAG	1119
QY	1107	CAG	AGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAGGATCGAGATG	1166
DB	1120	CAG	CATGCTATCTGAAGACAGATGAAGGATCTGATCTACCAAGAGGCTCTTGCATTC	1179
QY	1167	AA	CCCAACATCGGTA	1183
DB	1180	AA	CCCAAGATTACAGTA	1196

RESULT 8

AAC84262
 ID AAC84262 standard; cDNA; 1197 BP.

XX AAC84262;

XX AC (first entry)

XX 19-MAR-2001

XX Signal transduction protein encoding cDNA.
 XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
 XX auxin; cytokinin; gibberellin; immunogen; ss.

XX Zea mays.

Key	Location/Qualifiers
CDS	1..1197
FT	/*tag= a
FT	/product= "signal transduction protein"

XX WO200070059-A2.

XX 23-NOV-2000.

XX 28-APR-2000; 2000WO-US011687.

XX 14-MAY-1999; 99US-0134292P.

XX 08-JUL-1999; 99US-0142996P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Helentjaris TG;

XX WPI; 2001-031929/04.

XX P-PSDB; AAB48047.

XX New signal transduction nucleic acids and encoded proteins useful for
 XX regulating phytohormone expression, including ethylene, auxins,
 XX cytokinins and gibberellin, to provide control of plant response to
 XX environmental stresses.

XX Claim 1; Page 92-93; 126pp; English.

XX The invention provides Zea mays signal transduction proteins and encoding
 XX nucleotide sequences. The nucleic acids are useful for regulating
 XX expression of phytohormones, including ethylene, auxins, cytokinins, and
 XX gibberellin, to effect developmental changes in plants and provide
 XX control of plant response to environmental stresses. They may also be
 XX used as probes or amplification primers in the detection, quantitation or
 XX isolation of gene transcripts, for detecting mutations in the gene, for
 XX monitoring upregulation of expression or changes in enzyme activity in
 XX screening assays of compounds, for detection of any number of allelic
 XX variants, or for site-directed mutagenesis in eukaryotic cells. They may
 XX further be used for recombinant expression of their encoded polypeptides,
 XX as immunogens in the preparation or screening of antibodies, and in sense

CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a cDNA encoding a
CC signal transduction protein of the invention
XX
SQ Sequence 1197 BP; 306 A; 307 C; 292 G; 292 T; 0 U; 0 Other;

Query Match 36.6%; Score 511.2; DB 4; Length 1197;
Best Local Similarity 67.2%; Pred. No. 2.2e-95;
Matches 739; Conservative 0; Mismatches 358; Indels 3; Gaps 1;

QY 84 GGGCGCGCGTGGCGAGTTTCAGCGCGAGCATGACGACGCGCGCGTACCTGCTCTAC 143
DB 100 GCGGTGATGTTGGACAACATCCAGCGAGCGCTCAGCCACGGCGCGCTTCATCCAGTAC 159

QY 144 GACATCTTCGGGAACAAAGTTGAGAGTGAGCAACAGTACAGCGCGCGCATGATGCCCAT 203
DB 160 AACATCTTCGGCAACGTTTCGAGGTACCGCGCAAGTACAAAGCCCGCTCTCCCATC 219

QY 204 GCGCGCGCGCTACGCGATGCTGCTCGTGTGATGAATTTTGGAGAGGAGATGTTG 263
DB 220 GGCAGGCGCGCTACGCGATGCTGCTCGGCGCTCACTCCGAGAGCGGAGAGGTTG 279

QY 264 GCGATAAAGAGATGCGCAACGCGTTTCAACAACGACATGAGCGCCAGCGCATCGCTCCG 323
DB 280 GCCATCAAGAAGATGCGCAAGCGCTTCGACAACAAGATCGATGCCAAGCGCATCGCTCCG 339

QY 324 GAGATCAGCTCTCAGGCACTTCGACCGACGAGCAATCATAGGATCAGGGATGTGATC 383
DB 340 GAGATCAAGCTGCTCGGCCACATGAGCACGAGATATTTGTCATAAAGGGGAATCATA 399

QY 384 CCGCGCGCGATCCTCAGGCGTTCAACGAGCTTACATCGCCACGAGCTCATGGACAC 443
DB 400 CTTCTCGCGAGAGGCTGCAATTCATGATGTGTATATGTCATATGAATGATGGATCT 459

QY 444 GACCTCCATCATCATCTCCGCTCAACCAAGAACTGTCTAGAAGAGCACTGCCAGTATTTTC 503
DB 460 GATCTGATCAATATTCGTTCAATCAAGCTTTGTGAGAGGACACTGTCAAGTATTTT 519

QY 504 CTGTACAGATCTCGCGGGGCTCAAGTACATCACTCTCGCGCAACGTGATCCACCGGAC 563
DB 520 CTTTATCAATCTCTCGTGGCTTGAAGTATATACATTCAGCAATGTTCTTCAACCGTGAC 579

QY 564 CTGAGCGGAGCACTCTGCTGTAAGCGCAACTGCGACCTCAAGATCTGCGACTTCGGG 623
DB 580 TTGAGCCTAGCAATCTCTTTTGAATGCAAACTGTGACCTCAAGATATGTGATTTGGG 639

QY 624 CTGCGCGCGCGTCTGCGAGAGCGACATGATGACGGAGTACGTGGTCAACCGGTTGGTAC 683
DB 640 CTTGCTCGCACCACTCAGAACTGATTTTATGACTGAATATGTTGTCAAGATGGTAT 699

QY 684 CCGCGCGGAGCTGTGCTCAACTCAACGACTCTCGCGCGCATCGACGCTGTGGTCC 743
DB 700 AGAGCACAGAGCTTTTGTGAACTCTCAGAATATATCTGCTGCCATCGATGTGTGTCT 759

QY 744 GTGCGCTGCATCTTCAGGAGCTCATCAACCGCGCGCGCTCTTCCCGCAGGAGCCAC 803
DB 760 GTGGCTGTATATTTATGGAACCTGATGGACCGCAACCCCTGTGTTCTGGAAGAGACCAT 819

QY 804 ATGCACAGATGCGCTCATCACCGAGGTGATCGGACCGCGCGAGCGAGCTGCGGG 863
DB 820 GTCCATCAGCTACGCTCTTCAATGAGCTCATTTGGCAGCGCAATGAGGCTGATCTGAT 879

QY 864 TTCATACGGAACGAGGACGAGAGTACATGAGGCACTCGCGCGCATACCGCGCGCGG 923
DB 880 TTTTGTAAA--AATGAAAATGCAAGAAGATATATCCGCCAACTTCTCTGTCACCTAGACAG 936

QY 924 ACGTTGCGAGCATGTTTCCGCGGGTGCAGCCCGCGCTCGACCTCATTCGAGAGATG 983
DB 937 TCCTTACCTGAAAATTTCCACATGTATCAACCCCTTAGCAATGACCTGTGTGAAAAGATG 996

QY 984 CTCACCTTCAACCCGCTGACAGAAATCAAGTTGAGGAGCGCTCGATCATCTCTTACCTA 1043

DB 997 CTGACTTTTGATCTCTAGACAGAGAATAAAGTGTGAAGCGCACTTGCACACCCCTTACTTG 1056
QY 1044 GAGAGATTGACGACATCGCGATGAGCCCATCTGCTGGAGCCCTTCTCTTCCGACTTC 1103
DB 1057 GCATCATTATGATGATAGTATGAGCGAGGCTCTCAATGCCCTTCAGCTTTGACTTC 1116
QY 1104 GAGCAGAAGGCTCTAAACGAGGACCAAAATGAGCAGCTGATCTTCAACGAAGCGATCGAG 1163
DB 1117 GAGCAGCATGCTTCTGAGAACAAATGAGGATCTTATCTACCAAGAGGCTCTTGCA 1176

QY 1164 ATGAACCCAAACATCCGTA 1183
DB 1177 TTCAACCCCTGATTATCAGTA 1196

RESULT 9
AAC43105
ID AAC43105 standard; DNA; 1188 BP.
XX AAC43105;
XX AC
XX AAC43105;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38047.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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PR 09-AUG-1999; 99US-0147493P.
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PR 17-AUG-1999; 99US-0149175P.
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PR 20-SEP-1999; 99US-0154779P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 14-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match		36.4%;	Score 508.8;	DB 3;	Length 1188;
Best Local Similarity		67.2%;	Pred. No. 6.7e-95;		
Matches 736;		Conservative 0;	Mismatches 357;	Indels 3;	Gaps 1;
QY	92	GGTGGCGAGTTCAGCGCGAGATGACGACGCGCGCGTACTGCTCTACGACATCTT	151		
DB	96	GATTGAGAAATATTCGCGGAGCTCTTAGCCATGTGTGTAGTTTATTCAGTATTAACATAT	155		
QY	152	CGGGAACAAGTTCGAGGTGACGAACAAGTACCAAGCCGCCCATCATGCCATTTGGCGCGG	211		
DB	156	TGGAAACATCTTCGAGGTACCGCTAAGTATAAGCTCCGATCATCTATTGGCAAGG	215		
QY	212	CGCTTAGGGATGCTCTGCTCCGTGATGAATTTGAGACGAGGAGATGTGGCGATAA	271		
DB	216	TGCTTAGGCATCGTTTGTTCGGCTATGAATTTCTGAACTTAACGAGAGCGTTGCGATTAA	275		
QY	272	GAAGATCGCAACGCGTTTCAACAACGACATGAGCGCAAGCGCACCTCGGAGATCAA	331		
DB	276	GAATAATGCTAACGCTTTTGACAATAGATTTGATGCTTAAGAGGACTCTCCGTGAGATCAA	335		
QY	332	GCTCCTCAGGCACCTCGACCAAGAACATCATAGGCATCAGGGATGTGATCCCGCGGC	391		
DB	336	GCTGCTTCGTACATGGATCATGAATAATTTGTGCAATCAGAGATATTATCCGCGCAC	395		
QY	392	GATCCCTCAGGCGTTTCAACGAGCTTACATGCGCAAGAGCTCATGGAACAGCACTCCA	451		
DB	396	ATTAAGAAACGCTTTCAACGATCTTTACATCGCGTATGAGTTAATGACACTGATCTCCA	455		
QY	452	TCACATCATCCGCTCCAAACCAAGACTGTGAGAGAGCACTGCCAGTATTTCGTGACCA	511		
DB	456	TCAATATTCGCTCAATCAAGCATTTATCCGAAGAACATTTGCCAGTATTTTCTTTACCA	515		
QY	512	GATCCTCGCGGGCTCAAAGTACATCCACTCGCGCAAGCTGATCCACCGGACCTGAAGCC	571		
DB	516	GATCCTCGGTGATTGAATATACATTCACCTGCAATATGCTTCACAGGATTTGAACC	575		
QY	572	GAGCAACTGCTGCTGAAACGCAACTGCGACCTCAAGATCTGCGATCTCGGGTGGCGG	631		
DB	576	AAGTAATCTCTCTGAAACGCAACTGCGACCTTAAATAATCTGCGATTTTGGGTAGCTCG	635		
QY	632	CGCGTCTCGGAGGACATGATGACGAGTACGTGCTCACCCTGCTGACCGCGCC	691		
DB	636	AGTCACTTCGAGAGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG	695		
QY	692	GGAGCTGCTGCTCAACTCCACCGACTACTCGCGGCATCGAGCTCTGTGCTCGGCTG	751		
DB	696	AGAGCTTCTTAAACTCTTCTGATTATATCTGAGTATCGATGTTTGTCTGTAGGCTG	755		
QY	752	CATCTTCATGGAGCTCATCAACCGCGCGCTCTTCCCGGAGGAGCAACATGACCA	811		
DB	756	TATTTTTCATGGAGTTAATGGACGTAAGCCACTCTTCCCTGGACGAGATCATGTCATCA	815		
QY	812	GATGCGCTCATCACCGGTGATCGGAGCGCGAGCGAGCTGAGCTGGGTTCATAG	871		
DB	816	GCTTCGCTGCTCATGAGCTCATAGAACTCCATCAGAAAGAGCTGAGTTCTT---	872		
QY	872	GAACGAGGAGCGGAGGAATGATGAGGCACTTCGCGCAGTACCCGCGCGGACGTTCCG	931		
DB	873	GAACGAAGCGCAAGGATACATAGACAGCTTCCACCTTATCTTCGCAATCCATCAC	932		
QY	932	GAGCATGTTCCCGGGTGCAGCCCGCGGCTGCACTCATCGAGAGAGTCACTT	991		
DB	933	TGATAAGTTTCCCGACAGTGCATCTTTAGCTATAGACCTTATCGAAGATGTTTACAT	992		
QY	992	CAACCGCTGCAGAGATCACTGTCGAGGGGCTCGATCATCTTCTTACAGAGATT	1051		
DB	993	TGATCTTAGACGAGAGATCACTGTTTACAGCATTTGGCCCATTCATCTGAACTCGTT	1052		
QY	1052	GCAAGCATCGCGATGAGCCCATCTGCTGAGCGCTTCTCTCTGCACTTCGAGAGAA	1111		
DB	1053	GCACGACATAAGCGATGAGCGAGGTGTACAAATACCTTTCAACTTTGATTTTGAACCA	1112		
QY	1112	GGCTCTTAACGAGGACCAATGAAGCAGCTGATCTTCAAGAAAGCATCGAGATGAACCC	1171		

Db	1113	TGCACTCTCAGAGGAGCAGATGAAGAACTAATCTACCGCGAGCGCTTGCTTTCAATCC	1172	
QY	1172	AAACATCCGGTACTAG	1187	
Db	1173	AGAATATCAGCAATAG	1188	
RESULT 10				
ABZ12839				
ID	ABZ12839	standard; DNA; 1188 BP.		
XX	ABZ12839;			
XX	21-JAN-2003	(first entry)		
DE	Arabidopsis thaliana	stress regulated gene SEQ ID NO 644.		
XX	Arabidopsis thaliana;	plant; gene; stress; transgenic; ds.		
KW	Arabidopsis thaliana.			
OS	Arabidopsis thaliana.			
XX	WO200216655-A2.			
XX	28-FEB-2002.			
XX	24-AUG-2001;	2001WO-US026685.		
PP	24-AUG-2000;	2000US-0227866P.		
PR	26-JAN-2001;	2001US-0264647P.		
PR	22-JUN-2001;	2001US-0300111P.		
XX	(SCRI)	SCRIPPS RES INST.		
PA	(SYGN)	SYNGENTA PARTICIPATIONS AG.		
XX	Harper JF, Kreps J, Wang X, Zhu T;			
PI	WPI; 2002-304127/34.			
DR				
XX				
PT	Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.			
XX	Claim 144; SEQ ID NO 644; 577pp + Sequence Listing; English.			
XX	The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office			
XX	Sequence 1188 BP; 333 A; 273 C; 256 G; 326 T; 0 U; 0 Other;			
Query Match 36.4%; Score 508.8; DB 6; Length 1188;				
Best Local Similarity 67.2%; Pred. No. 6.7e-95;				
Matches 736; Conservative 0; Mismatches 357; Indels 3; Gaps 1;				
QY	92	GGTGGCGAGTTCAGCGCGAGATGACGACGCGCGGTACTGCTCTACGACATCTT	151	
Db	96	GATTGAGAAATATTCGCGGAGCTCTTAGCCATGTGTGTAGTTTATTTCAGTATTAACATATT	155	
QY	152	CGGGAACAAGTTCGAGGTGACGAACAAGTACCAAGCCGCCCATCATGCCATTTGGCGCGG	211	
Db	156	TGGAACATCTTCGAGGTACCGCTAAGTATAAGCTCCGATCATCTATTGGCAAGG	215	
QY	212	CGCTTAGGGATGCTCTGCTCCGTGATGAATTTGAGACGAGGAGATGTCGCGATATAA	271	

Db 216 TGCTTATGCGATCGTTTGTGCTATGATCTGAACTAACGAGCGTTGCGATTAA 275
 Qy 272 GAAGATGCGCAACGCTTCAACAAACGACATGAGCGCAAGCGCACGCTCGGAGATCAA 331
 Db 276 GAAATATGCTTAACGCTTTTGACAAATAGATGATGCTAAGAGGAGCTCTCGTGAGATCAA 335
 Qy 332 GCTCCTCAGGCACTCGACACGACATCATATGAGCATCAGGATGATGATCCGCGCC 391
 Db 336 GCTGCTCGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 395
 Qy 392 GATCCCTCAGGCGCTTCAACGACGCTTACATCGCGGAGCTCATGACACCGACCTCCA 451
 Db 396 ATTAAGAAACGCTTTCAACGATGTTTACATCGGATGATGATGATGATGATGATGAT 455
 Qy 452 TCACATCATCGCTTCAACCAACGACATGTCAGAAAGAGCTGCGAGATTTTCTGTACCA 511
 Db 456 TCAATCATTCGGTCAATCAAGCAATATCCGAAGAACATTTGCCAGTATTTTCTTTACCA 515
 Qy 512 GATCCTCGGGGCTCAAGTACATCCACTCGCGGACGTCATCCAGCGACCTGAAGCC 571
 Db 516 GATCCTCGGGGATGAATATACATCACTCTGCAATGCTTCAAGGATTTGAAACC 575
 Qy 572 GAGCAACCTGCTGCTGAACGCCAAGCTGCGACCTCAAGATCTGCACTTGGGCTGGCGG 631
 Db 576 AAGTAATCTCTCTGACGCAACCTGCGACCTTAAATCTGCAATTTGGGCTAGCTCG 635
 Qy 632 GCGCTCGTGGAGGAGACATGATGACGGAGTACGTTGTCACCGGTGTTACCGCGCC 691
 Db 636 AGTCACCTTCGAGAGTATTTCAATGATGATGATGATGATGATGATGATGATGATGAT 695
 Qy 692 GGAGCTGCTGCTCACTCAACCGACTACTCGCGGACGTCGATGCTGCTGCTGCTGCTG 751
 Db 696 AGAGCTTCTCTTAACTCTTCTGATATATCTGAGCTATGATGTTTGGTCTGAGCTG 755
 Qy 752 CATCTTCATGAGCTCATCAACCGCCAGCGCTCTTCCCGCGGAGGACACATGACACA 811
 Db 756 TATTTTCATGAGATTAATGACCGTAAAGCACTCTTCCCTGGACGAGATCATGTCCATCA 815
 Qy 812 GATCGCGCTCATCACCGAGTGTATCGGGACCGCGGACGACGAGCTGGGTTTCATACG 871
 Db 816 GCTTGGCTTCTCATGAGCTCATAGGACTCTCAAGCACTCCATCAGAAAGAGCTCGAGTCTT 872
 Qy 872 GAACGAGGACGAGGAGTACATGAGGACCTGCGCAGTACCGCGCGGAGCTTCGCG 931
 Db 873 GAACGAAACGCAAGCGATACATAGACAGCTTCCACCTTATCTCGGCAATCCATCAC 932
 Qy 932 GAGCATGTTCCCGGGTGACGCGCGCGCTCGACCTCATCGAGAGGATGCTCACTT 991
 Db 933 TGATAAGTTCGACAGTGCATCTTTAGCTATAGACCTTATCGAAGATGTTAATTT 992
 Qy 992 CAACCCGCTGCAGAGATCAAGTTGAGGAGCGCTCGATCATCTTACCTAGAGATTT 1051
 Db 993 TGATCTTAGAGGAGATCAAGTTTATAGAGCAATGAGGCACTTACCTGAACTCGTT 1052
 Qy 1052 GCAGCATCGCGATGAGGCGATCTGCTGAGGCGCTTCTCTTGAATTCAGAGCAAA 1111
 Db 1053 GCAGCATAGCGATGAGGCGAGTGTACAATACCTTTCAATCTTGAATTTGAAACCA 1112
 Qy 1112 GGCTCTAAACGAGCAACCAATGAGCAGCTGATCTTCAACGAGCGGATCGAGATGACCC 1171
 Db 1113 TGCACTCTAGAGAGAGATGAAGAACTAATCTACCGGAGCGCTTCTTCAATCC 1172
 Qy 1172 AAACATCCGGTACTAG 1187
 Db 1173 AGAATATCAGCATAG 1188

RESULT 11
 ADX47615
 ID ADX47615 standard; cDNA; 1637 BP.
 XX
 AC ADX47615;
 XX

DT 21-APR-2005 (first entry)
 XX Plant full length insert polynucleotide seqid 22355.
 DE plant protectant; plant growth regulant; gene therapy; plant;
 XX recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX Unidentified.
 OS US2004034888-A1.
 XX 19-FEB-2004.
 XX 28-APR-2003; 2003US-00425114.
 PF 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TAB/) TABASKA J E.
 PA (CAOV/) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 22355; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX Sequence 1637 BP; 420 A; 434 C; 381 G; 402 T; 0 U; 0 Other;
 SQ Query Match 35.3%; Score 492.2; DB 13; Length 1637;
 .Best Local Similarity 65.1%; Pred. No. 1.9e-91;
 Matches 725; Conservative 0; Mismatches 388; Indels 0; Gaps 0;
 QY 81 GACGGGCGCGCGTGGCGGAGTTTCAGCGCGACGATGACGCGCGCGGTTACCTGCTC 140
 Db 221 GCGGAGGAGGAGGAGGCGGAGTATGCGGACGACGCGGGGCGCGCTACGCTGCTG 280
 QY 141 TAGACATCTTCGGGAACAGTTTCGAGGTGACGAACAGTACCAGCGCCCATCATGCC 200

Db 281 TACAACTGTACGGGAACCTCTTCGAGGTCCTCCCAAGTACGCCCGGCCCATCCGCCCC 340
Qy 201 ATTGGCGCGCGCCCTTACCGGATCGTCTCGTCTCGTATGAACTTTTCAGACGAGGGAGATG 260
Db 341 ATCGCGCGCGCGCTACGGCAATGTCTCGCGCGTGTCAACTCACAGACAGGGAGGAA 400
Qy 261 GTGGCGATGAAGAAGATCGCAACGGGTTCAACACGACATGACGCCCAAGCGCAGCTC 320
Db 401 GTTGGCATCAAGAAGGTGGCAATGGCTTCGACACCAATCGACCGCAAGCGGAGCGTG 460
Qy 321 CGGGAGATCAAGCTCTCCAGGACCTCGACCGAGAAATCATAGCCATCAGGGGATG 380
Db 461 AGGGAGATCAAGCTCTCGCCACATGACCATGAGACATCTCTGCTTTAAGGACGTA 520
Qy 381 ATCCCGCGCGCGATCCCTCAGGCGTTCAACGAGCTCTACATCGCCACGAGGCTCATGGAC 440
Db 521 ATACGCGCCCACTAGAGAGAACTTTAATGACGTGTACATTGTTACTGAGTTAATGGAT 580
Qy 441 ACCGACTCTCATCATCATCTCCGCTCCACCAAGAACTGTGACAGACGACTGCCAGTAT 500
Db 581 ACAGATCTCCATCAGATCATACGCTCAAAATCAGCCATTGACTGATCATCTGCCAGTAC 640
Qy 501 TTCTGTACAGATCTCGGGGGCTCAAGTACATCCACTCGCGGAACGTGATCCACCGC 560
Db 641 TTCTGTATCAGTTGCTTGAAGGGCTTAAATATGTGCACTCAGCAATATATTTGACCGC 700
Qy 561 GACCTGAAGCGGAGCAACTGTCTGCTGAACGCACTCGGACCTCAAGATCTGCGACTTC 620
Db 701 GATCTAAAGCGGAGCAATTTGTTCTTAAATGCAATTTGTGACCTCAAGATCGCAGACTT 760
Qy 621 GGGCTGGCGCGCGCTGTGCGAGAGGACATGATGACGGAGTACGTGTCTACCCCGTGG 580
Db 761 GGGCTTTCAGGAGCACTCCTCAGAGACAGATCTCATGACAGAGTATGTGTCTACTCGTTG 820
Qy 681 TACGCGCGCGGAGCTGTCTCACTCCACGACTACTCGCGCGCCATCGAGCTG 740
Db 821 TACAGGCGCAGAGCTGTCTGTTGAATCTGTTACAGTACACTGCTGCCATTGATGTCTG 880
Qy 741 TCGCTCGGCTGCATCTTCATGAGCTCATCAACCGCGAGCGCTCTTCCCGCGAGGAC 800
Db 881 TCAGTTGGATGCATATTAGGTGAATCGTTACTCGCCAAACCTGTTTCTCGACGGAT 940
Qy 801 CATGACACAGATGCGCTCATCAGGAGTGTATCGGGACGCGGAGGACGAGCTG 860
Db 941 TACATCCAGCAGTTAAATTTGATCAGCGAGCTCATAGGCTCACCAGATGATCAAGCCTG 1000
Qy 861 GGGTTTCATACGGAACGAGGACGAGGAGTACATGAGCACTGCGCAGTACCCGCGC 920
Db 1001 GGAATTTCTGAAAGTGAATATGCAAAAGATACATGAACAACATACACAGTTTCCAAG 1060
Qy 921 CGGACGTTTCGCGAGCATGTTCCCGCGGGTGCAGCCGCGCTCGACCTCATCGAGAGG 980
Db 1061 CAGGACTTCGCGCTGCGTTTCCGTAACATGCTCTCTGCTGCTGATGTTGGAGAGA 1120
Qy 981 ATGCTACCTTCAACCGCTGACAGAAATCAGAGTTGAGGAGCGCTCGATCATCTTAC 1040
Db 1121 ATGCTGTGTGTTGATCCAAAGCAGACGGAATACAGTTGATGAGGCTCTGCACTACCCATAC 1180
Qy 1041 CTAGAGAGATTCACGACATTCGCGATGAGCCCATCTGCTGAGCGCTTCTCTTCGAC 1100
Db 1181 TTGGCTTCACTTCATGACATCAATGAGAAACCTTACTGCTGCACTTTTACGTTTGTAT 1240
Qy 1101 TTCGAGCAGAAGGCTCTTAAACGAGGACCAATGAAGCAGCTGTATCTTCAACGAGCGATC 1160
Db 1241 TTTGAGCAACCATCTTTTACAGAAGCGCATATAAAGAACTTATCTGGAGGAATCTTTA 1300
Qy 1161 GAGATGAACCAACATCCGGTACTAGATTGAA 1193
Db 1301 GCATTTAACCCGATCTCTCCCTACTAATTTCAA 1333

RESULT 12
ADXS3699

ID ADXS3699 standard; cDNA; 1520 BP.
XX AC ADXS3699;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 28439.
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX XX 28-APR-2003; 2003US-00425114.
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI; 2004-180133/17.
XX XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX PS Claim 1; SEQ ID NO 28439; 15pp; English.
XX CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 1520 BP; 393 A; 351 C; 367 G; 409 T; 0 U; 0 Other;
Query Match 34.8%; Score 485.8; DB 13; Length 1520;
Best Local Similarity 64.8%; Pred. No. 3.8e-90;
Matches 721; Conservative 0; Mismatches 392; Indels 0; Gaps 0;
QY 81 GACGGGGCGCGGTGCGGAGTTTCAGCGCGGAGTACGACGCGCGGTACCTGCTC 140

Db 38 GGGGGCGGCTGGAGCGCAGATCAAGGGTATGGCGACGCA CGGGGGCGCTACGTGCTG 97
Qy 141 TAGACATCTTCGGGAAAGTTTCGAGGTGACGAACAAGTACGAGCGCCCATCATGCCC 200
Db 98 TACACGTGTAGGGAACTCTTCGAGGTCTCTCCAGTACGCGCCCACTCCGCC 157
Qy 201 ATTGGCGGCGGCTTACGGGATCGTCTGCTCCGTGATGAATCTTGAGAGGAGGATG 260
Db 158 ATCGGTGCGGGCGCTTACGGCATTTGTCTCGGGCTGTCACTCGCAGTCAGGGAGGAG 217
Qy 261 GTGGCGATAAAGAGATCGCAACGCTTCAACACGACATGACGCCCAAGCGCAGCTC 320
Db 218 GTTGCAATCAGAGGTTGGCAATGCTTGCACACCAATCGACGCCAAGCGGAGCTC 277
Qy 321 CGGGAGATCAAGCTCTCAGGCACTCGACCGAGAAATCATATAGGCATTCAGGGATG 380
Db 278 AGGGAATCAAGCTGTGGCCACATGACCAATGAGAAATCTTGCCTTAAAGGATGA 337
Qy 381 ATCCCGCGCGGATCCCTCAGGGGTTCAAGAGGTCTACATCGCCAGGAGCTCATGGAC 440
Db 338 ATTCGGCCCCCACTAGAGAGAACTTTAATGAGGTGATCAATTTACTGAGTTAATGGAT 397
Qy 441 ACCGACTCATCATCATCTCCGCTCCAAACCAAGAACTGTCAAGAGCACTGCCAGTAT 500
Db 398 ACAGATCTCCATCAGATCGTACGCTCAATCAGCCATTGACTGATGATCATTTGCCAGTAC 457
Qy 501 TTCCTGTACAGATCTCGGGGGCTCAAGTACATCCATCTCGGCGAACTGATGCCACCG 560
Db 458 TTTCTGTATCAGTTGTTACGAGGGCTAAATATGTGCACTCAGCAAAATATATTGCCACCG 517
Qy 561 GACCTGAGCGGAGCAACTGCTGTGAACGCCAACTCGGACCTCAAGATCTCGGACTTC 620
Db 518 GATCTGAAGCGGAGCAATTTGTTCTTAAATGCAAAATTTGACCTCAAGATTGAGACTTT 577
Qy 621 GGGCTCGGCGGCGCTGTCGAGAGCGCATCATGACGAGTACGTGGTCAACCGGTG 680
Db 578 GGGCTTGCAGAGCACTTCAGAGACAGATCTCATGACAGATATGTGTCATCTCTTGG 637
Qy 681 TACCGCGCGGAGCTGTCTCAACTCAGCACTACTCGCCGCCATTCGACGTCTG 740
Db 638 TACCGGCGCACGAGCTGCTTTGAATGTTTACAGTATCTGCTGCCATTGATGCTG 697
Qy 741 TCGCTCGGCTGATCTTCATGAGCTCATCAACCGCGAGCGCTCTTCCCGCGCAGGAC 800
Db 698 TCAGTTGGATGTCATCTAGTGAAATCGTTACTCGTCAACCCCTGTTCTCGGACGGAT 757
Qy 801 CACATCACCAGATCGCCTCATCACGAGTGTATCGGACCGCGAGCGGACGAGCTG 860
Db 758 TACATCAGCAATTAATTTGATCTATGAGCTCATAGGCTCTCCAGATGATGAGCCTG 817
Qy 861 GGGTTTCATACGAGGAGCGGAGAGTATCATGAGGCACCTGCGCAGTACCCGCGC 920
Db 818 GGATTTCTTCAAGTATGATGCAAAAGATACATGAACAACCTACCAAGTTTCCAAGA 877
Qy 921 CGGAGCTTCGAGAGATGTTCCGCGGGTGCAGCGCCGCGCTCGACCTCATCGAGAG 980
Db 878 CAGGACTTCGCGCTGCGCTTTCCGCAACATGTCTCTGGCGCAGTCGATTTGTTGAAAG 937
Qy 981 ATGCTACCTTCAACCGCTGCAGAGAAATCACAAGTTGAGGAGCGCTCGATCATCTTAC 1040
Db 938 ATGCTTGTGTTGATTCAGCAGACGGATTTACAGTTGATGAGGCTCTGCATCATCCATC 997
Qy 1041 CTAGAGAGATTGACGATCGCGGATGAGCCCATCTGCTTGGAGCGCTTCTCTTCGAC 1100
Db 998 TTGGCTTCACTTCATGAGATCAATGATGAACCTACCTGCCCTGCACCTTTTCAGCTTGT 1057
Qy 1101 TTGAGCAGAGGCTTAAACGAGGACCAATGAGCAGCTGATCTTCAACGAGGATC 1160
Db 1058 TTTGAGCAACCATCTTTTACAGAGCGCATATAAAGAACTCATCTGGAGGGAATCTTTA 1117
Qy 1161 GAGATGAACCAACATCCGGTACTAGATTGAA 1193
Db 1118 GCATTTAACCCAGAGCCTCCCTACTAATATCAA 1150

RESULT 13
AAC43674
ID AAC43674 standard; DNA; 1546 BP.
XX AC AAC43674;
XX DT 18-OCT-2000 (first entry)
XX Zea mays DNA fragment SEQ ID NO: 40086.
DE Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic; pathway;
KW promoter; termination sequence; corn; ss.
XX Zea mays subsp. mays.
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
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PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
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PR 24-MAY-1999; 99US-0135629P.
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PR 04-JUN-1999; 99US-0137502P.
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Qy 261 GTGCGGATTAAGAAGATCGCAACGGGTTTCAACAGCAGATGAGCGCCAGCCAGCCGCTC 320
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Qy 321 CGGAGATCAAGCTCTCCAGCGACCTCGACCGAGAACATAGGACATAGGAGATG 380
Db 396 AGGGAATCAAGCTCTCGCCACATGACCATGAGAACTCTTGGCTTTAAAGGATGTA 455
Qy 381 ATCCGCGCGCGATCCCTCAGGGGTTTCAACGAGTCTTACATCGCCACGAGCTCATGGAC 440
Db 456 ATTCCGCCCCCACTAGAGAGAACTTTAATGACGTGTACATTGTACTGAGTTAATGAT 515
Qy 441 ACCGACTCATCATCATCTCCGCTCAACCAAGAACTGTTCAGAAAGCACTCCGAGTAT 500
Db 516 ACAGATCTCCATCAGATCGTACGCTCAAAATCAGCCATTTGACTGATCATATTGCCAGTAC 575
Qy 501 TTCCTGTACAGATCTCTCGGGGCTCAAGTACATCCACTCGCGCAACGTGATCCACCGC 560
Db 576 TTTCTGTATCAGTTGTTACGAGGCTAAATATATGTGCACCTCAGCAATATATTGCAACCGC 635
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Qy 741 TCGCTCGGCTGCATCTTCATGAGCTCATCAACCGCGAGCGCTCTTCCCGCGCAGGAC 800
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Qy 801 CACATGACAGATGCGCCCTCATCACCGAGGTGATCGGAGCGCGGACGCGAGCAGAGCTG 860
Db 876 TACATCCAGCAATTAATAATTGATCACTGAGCTCATAGGCTCTCCAGATGATGCAAGCCTG 935
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Qy 921 CGGACGTTTCGCGAGCATGTTCCCGGGGTGCGCGCGCTCGAGCTTCGACCTCATCGAGAGG 980
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Qy 1101 TTCAGCAGAAGGCTCTTAAACGAGGACCAATGAGCAGCTGATCTTCAACGAGCGATC 1160
Db 1176 TTTGAGCAACATCTTTACAGAGCGCATATAAAGAACTCATCTCGAGGGATCTTTA 1235
Qy 1161 GAGATGAACCAACATCCGCTACTAGATTGAA 1193
Db 1236 GCATTTAACCCAGAGCCTCCCTACTAATATCAA 1268
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RESULT 14
AAV2563
ID AAV2563 standard; cDNA; 1544 BP.
XX
AC AAV2563;
XX

```
DT 22-SEP-1998 (first entry)
XX Salicylic acid induced MAP kinase encoding cDNA.
DE Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
XX Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
KW tobacco; disease resistance; microbial pathogen; MAP kinase; ds.
XX Nicotiana sp.
XX Key Location/Qualifiers
CDS 129..1310
FT /tag= a
FT /product= "salicylic acid induced MAP kinase"
XX
XX W09818939-A1.
XX 07-MAY-1998.
XX 24-OCT-1997; 97WO-US019219.
XX 25-OCT-1996; 96US-002980SP.
PR 21-APR-1997; 97US-00837593.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX Klessig DP, Zhang S;
PI WPI; 1998-272230/24.
XX P-PSDB; AAW61252.
XX Salicylic acid induced MAP kinase - obtained from tobacco, used to
PT produce plants having increased disease resistance, against e.g.
PT microbial pathogens.
XX Claim 11; Page 21-22; 97pp; English.
XX This cDNA encodes a salicylic acid induced protein (SIP) kinase. This SIP
CC kinase is an unique member of the mitogen-activated protein (MAP) kinase
CC family. The salicylic acid induced MAP kinase of the invention comprises
CC kinase subdomains I to XI of serine/threonine kinases. The protein is
CC activated by an agent that induces a disease response in plants
CC by way of a signal transduction pathway that is at least partially
CC dependent on salicylic acid. Host plant cells transformed with a vector
CC containing a recombinant DNA molecule encoding the salicylic acid induced
CC MAP kinase is used to produce the protein recombinantly. The products can
CC be used to produce plants with increased disease resistance. The products
CC may also be used as a research tool to identify other proteins involved
CC in the hypersensitive response and systemic acquired response in plants
XX
SQ Sequence 1544 BP; 449 A; 294 C; 335 G; 466 T; 0 U; 0 Other;
Query Match 34.7%; Score 484; DB 2; Length 1544;
Best Local Similarity 65.6%; Pred. No. 9e-90;
Matches 722; Conservative 0; Mismatches 375; Indels 3; Gaps 1;
Qy 84 GGGGCGCGGTGCGGAGTTTCAGCGCGACATGACCGCGCGGCGGCTGCTCTAC 143
Db 207 GTGCGCGGTATGATAATATTCGCGCGACGTTTCAGCGCGGCGGCTGCTCTAC 266
Qy 144 GACATCTTCGGGAACAAGTTTCGAGGTGAGCAACAGTACCAGCGCGCCCATGCCCAT 203
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Qy 324 GAGATCAAGCTCTCAGGCGACCTTCGACCGAGCAATCATAGGCATCAGGATGTCATC 383
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Db 447 GAGATCAAGCTTCTTCGGCATATGGATCATGAACAATTTGTCGATCAGAGATATAATT 506
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Db 507 CCACCAACACAGAGAGAGCGCTTAATGATGTTTATATGATGTTTATGCGTATGAGCTTATGGATCT 566
Qy 444 GACCTCCATCACAATCATCGCTCCAAACCAAGAACTGTGAGAGAGAGCACTGCCAGTATTTTC 503
Db 567 GATCTCCATCAAAATTTTCGCTCTAATCAGGGTTTATCTGAGGAGCACTGTGATATTTTC 626
Qy 504 CTGTACACAGATCTCGGGGGGCTCAAGTATACATCCACTCGCGGAACTGTATCCACCGGAC 563
Db 627 TTGTATCAGATCTCCGAGGTTGAAATACATATCTGCGAATGTTCTGCACAGGAG 686
Qy 564 CTGAAGCCGAGCAACTGTCTGTAAGCGCACTGCGACCTCAAGATCTGCGACTTTCCGG 623
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Qy 1044 GAGAGATTGACACATCGCCGATGAGCCCATCTGCTGAGGCCCTTCTCTTGCATCTC 1103
Db 1164 AACTCGCTCCAGCATATTATGACGAGCCCATTTGCATGACTCCCTTTAGCTTTCGACTTT 1223
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Qy 1164 ATGAACCCAAACATCCGGTA 1183
Db 1284 TTTAATCCTGAATACCAGCA 1303

RESULT 15

AAc84253
ID AAC84253 standard; cDNA; 1119 BP.

AC AAC84253;

XX 19-MAR-2001 (first entry)

DT Signal transduction protein encoding cDNA.

DE Zea mays; maize; signal transduction protein; phytohormone; ethylene;
KW auxin; cytokinin; gibberellin; immunogen; ss.

XX Zea mays.

XX Key Location/Qualifiers
FH 1..1119
FT /*tag= a
FT /product= "signal transduction protein"
XX
FN WO200070059-A2.
XX
PD 23-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011687.
XX
PR 14-MAY-1999; 99US-0134292P.
PR 08-JUL-1999; 99US-0142996P.
XX (PION-) PIONEER HI-BRED INT INC.
XX Helentjaris TG;
XX WPI; 2001-031929/04.
DR P-PSDB; AAB48044.
XX
PT New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses.
XX Claim 1; Page 83-85; 126pp; English.
XX
CC The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins, and
CC gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a cDNA encoding a
CC signal transduction protein of the invention
XX
SQ Sequence 1119 BP; 290 A; 282 C; 268 G; 279 T; 0 U; 0 Other;
Query Match 34.6%; Score 483.6; DB 4; Length 1119;
Best Local Similarity 64.8%; Pred. No. 1e-89;
Matches 717; Conservative 0; Mismatches 389; Indels 0; Gaps 0;
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Db 13 GCGCGCGCGGTGGAGCGCAGATCAAGGGTATGGCGACGACGCGGGCGGCTACGTGCTG 72
Qy 141 TACGACATCTTCGGGACAAAGTTTCAGGTGAGAAACAGTACAGCCGCTCATGCCCC 200
Db 73 TACAACGTTAGCGAAACCTCTTCGAGGTCTCTCAAGTACGCCACCACTCCGCCCC 132
Qy 201 ATTGGCCGCGCGCTTACGGGATCGTCTGCTCGTGATGAACCTTTTGAGACGAGGGAGATG 260
Db 133 ATCGGTTCGCGCGCTTACGGCATTTGTCTGCGGGCTGTCAACTCGCAGTCAGGGAGGAG 192
Qy 261 GTGGCGATTAAGAAGATCGCCAAACCGGTTCAACAAGCATGAGACGCCAAGCGCGCTC 320
Db 193 GTTGGCATCAGAAGGTTGGCAATGCGTTTCGAAACCAACATGACGCGCAAGCGCGCTC 252
Qy 321 CGGGAGATCAAGCTCTCTCAGGCACCTCCGACACGAGAACATCATAGGCATCAGGAGTG 380
Db 253 AGGGAATCAAGCTCTCTGCGCCACATGGACCATGAGAACATCTTTCCTTTAAGGATGA 312

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	483.2	34.6	1725	3	US-09-623-034-1
3	444	31.8	1718	3	US-09-828-313-21
4	337.2	24.2	1866	3	US-08-909-742-1
5	337.2	24.2	1866	3	US-09-412-289-1
6	337.2	24.2	1896	3	US-09-417-197-38
7	334	23.9	1875	3	US-09-417-197-56
8	319.8	22.9	953	3	US-09-828-313-8
9	318	22.8	1747	2	US-08-176-620A-1
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11	318	22.8	1747	2	US-08-461-985-1
12	318	22.8	1747	2	US-08-458-887-1
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14	318	22.8	1747	3	US-08-932-012C-1
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18	312.2	22.4	2980	3	US-09-266-225D-11
19	292.6	21.0	1502	2	US-08-651-940-1
20	292.6	21.0	1502	3	US-09-295-029-1
21	292.6	21.0	1502	3	US-09-724-768-1
22	291	20.8	1134	3	US-09-949-016-3997
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24	289.6	20.7	1310	3	US-08-802-191-1

25	288.6	20.7	1457	3	US-09-949-016-3988
26	279.2	20.0	1851	2	US-08-674-612-1
27	279.2	20.0	1851	2	US-08-700-575-45
28	279.2	20.0	1851	2	US-08-920-296-1
29	279.2	20.0	1851	3	US-09-124-163-1
30	278.8	20.0	1095	3	US-09-809-464-2
31	278.8	20.0	1259	3	US-09-809-464-3
32	278.8	20.0	1839	3	US-09-949-016-5420
33	276.8	19.8	1834	3	US-09-016-434-419
34	274.8	19.7	1260	2	US-08-029-404-1
35	274.8	19.7	1260	3	US-08-459-953A-1
36	274.8	19.7	1260	3	US-08-746-788-1
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38	273.6	19.6	1838	3	US-09-189-602-1
39	265	19.0	2180	3	US-09-286-904-23
40	265	19.0	2180	3	US-09-646-101-23
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42	258	18.5	1611	3	US-08-909-742-2
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44	258	18.5	1701	3	US-09-949-016-4048
45	258	18.5	1701	3	US-09-016-434-1263

ALIGNMENTS

RESULT 1
US-08-837-593-1
; Sequence 1, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1544 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

FRAGMENT TYPE:
ORIGINAL SOURCE: tobacco
US-08-837-593-1

Query Match 34.7%; Score 484; DB 2; Length 1544;
Best Local Similarity 65.6%; Pred. No. 5.4e-97;
Matches 722; Conservative 0; Mismatches 375; Indels 3; Gaps 1;

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QY 84 GGGCGCGCGTGGCGGAGTTTCAGGCGGACGATGACGACGCGCGCGGTACCTGCTCTAC 143
DB 207 GTGGCCGGTATGATTAATATTCGGCGAGCTTGAGCCACGGTGGCGAGGTTCAATCAATAC 266

QY 144 GACATCTTCGGGAACAAGTTTCGAGGTGACGAAACAAGTACCAGCGGCCCATCATGCCATT 203
DB 267 AATATATTTGGTAATATATTTGAAGTTACTGCTAAATATAAGCTCTATTTTGCCTATT 326

QY 204 GGGCGCGCGCTTACGGGATCGTCTGCTCGGTGATGAATTTGAGACGAGGAGATGGTG 263
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QY 384 CGCGCGCGATCCCTCAGGGTTCAACGAGTCTATCGCCACGAGGCTCATGACACC 443
DB 507 CCACCAACACAGAGAGGCGCTTAAATGATGTTTATATTTGCGTATGAGCTTATGGATCT 566

QY 444 GACCTCCATACATCATCGCTCCCAACCAAGAACTGTCAGAAAGACGACTGCCAGTATTT 503
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QY 744 GTGCGTGTGATCTTTCATGAGCTCATCAACCGCGAGCGCTCTTCCCGCGAGGAGCAC 803
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QY 1164 ATGAACCCAAACATCCGGTA 1183
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RESULT 2
US-09-623-034-1
; Sequence 1, Application US/09623034
; Patent No.: 6765128
; GENERAL INFORMATION:
; APPLICANT: Klesbig, Daniel F.
; APPLICANT: Zhang, Shuhun
; TITLE OF INVENTION: METHODS OF USING A PATHOGEN-ACTIVATABLE
; FILE REFERENCE: RUT98-0073
; CURRENT APPLICATION NUMBER: US/09/623,034
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/03882
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 60/075,685
; PRIOR FILING DATE: 1998-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-623-034-1

Query Match 34.6%; Score 483.2; DB 3; Length 1725;
Best Local Similarity 65.3%; Pred. No. 8.4e-97;
Matches 710; Conservative 0; Mismatches 378; Indels 0; Gaps 0;

QY 84 GGGCGCGCGTGGCGGAGTTTCAGGCGGACGATGACGCGCGCGGTACCTGCTCTAC 143
DB 141 GGAGGTCAATTCCTCGATTTTCTTCGGTTTAACTCACGCGGCAATATGTACAGTTT 200

QY 144 GACATCTTCGGGAACAAGTTCGAGGTGACGAAAGTACCAGCGGCCCATCATGCCATT 203
DB 201 GATATTTTGGTAATTTCTTTGAGATCACTACCAAGTATCGTCTCTTATATGCTATT 260

QY 204 GGGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAATTTTGAGACGAGGAGATGGTG 263
DB 261 GGTCTGCTGGTCTTATGGAATTTGCTGCTCGGTGTTGAATACGAGCTGAATGAGATGGTT 320

QY 264 GGGATAAAGAGATCGCCCAACGCGTTCAACAACGACATGAGCGCCCAAGCGCGCTCCGG 323
DB 321 GCAGTTAAAGAAATTCGGAATCGGTTTGATATTTACATGGATGCTTAAGAGGACTCTCCGT 380

QY 324 GAGATCAAGCTCTCAGGCACTCGACCAACGAGAACATCATAGGATCATAGGATGTGATC 383
DB 381 GAGATTAAGCTCTCTCCGCCATTTAGACCATGAAATGTAATTTGTTTAAAGACGCTGATT 440

QY 384 CGCGCGCGCGATCCCTCAGGCGTTCAACGACGCTCTACATCGCCACGAGGCTCATGGACACC 443
DB 441 CCTCCACCTTACGAAGGAGTTTCTCTGATGTTTACATTTGCTACTCTGAACTCATGTACT 500

QY 444 GACCTCCATCATCATCATCGCTCCCAACGAGAACTGTGAGAAAGACACTGCCAGTATTC 503
DB 501 GATCTTTCACCAATTAATTAAGATTCACCAAGGTTTATCAGAGGATCACTGTGACTTTC 560

QY 504 CTGTACCAAGATCTCGCGGGGCTCAAGTATCATCTCGCGCAAGCTGATCCACCGCGAC 563
DB 561 ATGATCAGCTCTCTCCGCTGGCGCTAAATACATACATCTTCGCGAATGTTCTTCATAGAT 620

QY 564 CTGAAGCCGAGCAACCTCTGCTGTAACGCCAACTGCGCACTGCAAGATCTGCGAGTTCGGG 623
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[illegible]

RESULT 3

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US-09-828-313-21
; Sequence 21, Application US/09828313
; Patent No. 6867351
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, RUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1718
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-21

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Query Match 31.8%: Score 444: DB 3: Length 1718:

Query Match 31.8%; Score 44%; DB 3;
Best Local Similarity 63.9%; Pred. No. 3.5e-88;

Matches 672; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

Qy	111	ACGATGACGCA	CGCGCGCGTAC	CTGCTTACGAC	CATCTTCGGGAA	CAAGTTCGAGTG	170							
Db	424	ACTCCGACCT	ACGAGGCTCA	TACGTTGA	ATAATGTTGTCGCGGAA	CTGATTTCGAAGTC	483							
Qy	171	ACGAACAAGT	PACAGCGGCC	CAATCATGCC	CAATTTGGCGCGGCGCCT	PACGGATCGTCTGC	230							
Db	484	ACCGGAGGT	PACAGGCCA	CACTTCTGTC	CGATTTGGCGCGGAGCTT	ATGGAATCGTCTGT	543							
Qy	231	TCGCTGAT	GAACTTTTGAG	ACGAGGAGAT	GTGGTGGCGAT	TAAGAAGATCGCCAA	CGGTTTC	290						
Db	544	TCACTCTT	TGATACCGT	TACGGGT	GAGGAGTGGCGGT	CAAAAAGATGGA	ACGCTTC	603						
Qy	291	AACAACG	ACATGGA	CGCCAA	CGCGACGCTCCG	GAGATCAAGCTCTCT	CAGGCACTCGAC	350						
Db	604	GACAA	CAGGATCG	ATGCGAAGCG	CACTCGCTGAAAT	TAATACTCTCCG	GCATATGGAT	663						
Qy	351	CACGAGAA	CATCATAGG	CAATCAGG	ATGTGATCCCGCGCGAT	CCCTCAGGCGTTCA	CAAC	410						
Db	664	CATGA	AAACGTGCTGCC	CAATACAG	ACATCATTTGTC	CCCCCACTAGG	GAGAAATTTCA	723						
Qy	411	GAGCTCT	CATGCCAC	CGAGCTCAT	GTGACACG	CACTCCATCA	CTCATCTCCGCTCCA	CAAC	470					
Db	724	GAGTGT	CATTTGTAT	ACGATTG	ATGATACG	GACTACAC	CAGATCATTTCTGTTCAA	AT	783					
Qy	471	CAAGAA	CTGT	CAGAAG	CACTGCCAGT	ATTTCTCTGTAC	AGATCTCTGCGGGGCTCA	AG	530					
Db	784	CAAGCT	CTCAC	GAAGAC	CACTGT	CAGTATTTCTGTAT	CAAAATCTTTCGCGGCTTGA	AG	843					
Qy	531	TACAT	CTC	TGCGGAA	CGTGATC	ACCGGCACTG	AGCGCGAGCA	CACTGCTCTGCTGA	AC	590				
Db	844	TACAT	CCATTT	TCGCGCA	ACGCTTTTG	CAACCGGACTTTGA	AGCCCAACCTTCTCTG	CTCAAT	903					
Qy	591	GCCAA	CTGGCA	CTCAAG	ATCTCG	CACTTCGCGCGCGCTG	CTCGGAGAGCG	CAAC	650					
Db	904	GCCAA	TTGCGATTTG	AAATCG	CAGATTTTGG	CTTTGGCA	CGCACTCTCTCTG	GAACCG	AT	963				
Qy	651	ATGAT	GACGAGT	ACGTGGT	CACCCGCTGT	TACCGCGCGCGGAGCTG	CTGCTCA	ATCC	710					
Db	964	TTCA	TGACTG	ATGTTGT	TGTAA	CGAGTGTGTAC	GAGCTCCAGAGCTGCTCCTG	GAATGT	1023					
Qy	711	ACGCA	CTACT	TCGCGG	CACTCG	ACGTCTG	GTCTGCGCTG	CAATCTT	CATG	GA	CT	CA	TC	770
Db	1024	TCAGCA	TACACT	CGAGCT	ATTG	CACTTTGGT	CTGTGCGG	GTGCATCTTT	CATG	GA	TTG	CTT	1083	
Qy	771	AACG	CGCACCGCTCT	CCCCG	CAGGACCA	CATG	CAACAGATG	CGCCTCAT	CA	CCG	AG	830		
Db	1084	AACCG	ATCTG	CTGTTGTTCC	CTGGAGAG	ACTATGT	GCATCAGCT	TCG	CCCTTAA	TTAC	GAA	1143		
Qy	831	GTGAT	CGGACG	CGGACG	AGCTGG	GTTCAT	ACGAA	ACGAGG	ACGCGAG	CAAG	890			
Db	1144	CTCAT	CGAACTCT	GTGA	GATAGG	ATCTTGG	GTGTTT	TGAG	AGGCA	ATGCTAG	CGG	1203		
Qy	891	TACAT	GAGG	CACT	TCGCG	CACTAC	CGCGCGG	ACGTTTC	CGGAG	CAATGTTCC	CGCGGGT			

```

RESULT 4
US-08-909-742-1
; Sequence 1, Application US/08090742
; Patent No. 6007991
; GENERAL INFORMATION:
; APPLICANT: Vimala S. Sivaraman
; APPLICANT: Helen-Yu Wang
; APPLICANT: Craig C. Malbon
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
; TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,742
; FILING DATE: August 12, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,994
; FILING DATE: April 1, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,520
; FILING DATE: March 28, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Adams, Lindsey S.
; REGISTRATION NUMBER: 36,425
; REFERENCE/DOCKET NUMBER: 178-225 CIP II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1866 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-909-742-1

Query Match 24.2%; Score 337.2; DB 3; Length 1866;
Best Local Similarity 61.3%; Pred. No. 1.1e-64;
Matches 603; Conservative 0; Mismatches 363; Indels 18; Gaps 3

QY 182 CCAGCGCGCCATCATGCCCATTTGGCCGGCGGCGCTACGGGATCGTCTGCTCCGTGATGAA 241
DB 195 CTACAGCATGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGTGTACAGCTCGGCCTATGA 254
QY 242 CTTTGTAGACGAGGGAGATGGTGGCCATAAAGAAGATCGCCAAACGCGTTCAACACGACAT 301
DB 255 CCACGTGGCGCAAGACTCGCGTGGCCATCAAGAGAT---CAGCCCTTCGAACATCAGAC 311
QY 302 GGACGCCAAGCGAGCGTCTCGGGAGATCAAGCTCTCAGGCACTCTGACCAACGAGAACAT 361
DB 312 CTACTGCCACGCGACGCTCCGGAGATCCAGATCCTGCTGCGCTTCGCGCATGAGAATGT 371
QY 362 CATAGGCATCAGGATGTATCCCGCGCGCATCCCTCAGGCGTTCAACGACGCTCTACAT 421
DB 372 CATCGGCATCCGAGACATTTCTGCGGGCGGTCCACCTTGGAAAGCCATGAGAGATGTCTACAT 431
QY 422 CGCCAGGAGCTCATGGACACCGACCTCCATCACATCATCGCTCCCAACCAAGAACTGTC 481

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; SEQ ID NO 1
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-412-289-1

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Query Match	24.2%; Score 337.2; DB 3; Length 1866;
Best Local Similarity	61.3%; Pred. No. 1.1e-64;
Matches 603; Conservative	0; Mismatches 363; Indels 18; Gaps 3;
182	CCAGCCGCCCATCATGCCAATTGGCCGCGCGCTACGGGATCGTCTGCTCGTGATGAA 241
Db	
195	CTACACGAGTTGCAGTACATCGGCGAGGGCGGTACGGCATGCTCAGTTCGGCCTATGA 254
Db	
242	CTTTGAGACGAGGGAGATGGTGGCGATAAAGAAAGATCGCCAAACGCGTTCAACAACGACAT 301
Db	
255	CCACGTTGCGCAAGACTCGGTGGCCATCAAGAAAT---CAGCCCTTCCAAATCAGAC 311
Db	
302	GGACGCCAAGCAGCAGCTCGGGAGATCAAGTCTCTCAGGCACCTCGACCGAGAAACAT 361
Db	
312	CTACTGCCAGCGCACGCTCGGGAGATCCAGATCTCTGCTGCGCTTCGCGCATGAGAATGT 371
Db	
362	CATAGGCATCAGGGATGTGATCCGCGCGCGATCCCTCAGGCGGTTCAAAGCACTCTACAT 421
Db	
372	CATCGGATCCGAGACATTTCTGGGGGTTCCACCTGGGAAGCATGAGAGATGTTACAT 431
Db	
422	CGCCACGGAGCTCATGGACACCGACCTCCATCAATCATCTCCGCTCCAAACCAAGAACTGTC 481
Db	
432	TGTGCAGGACCTGATGGAGACTGACCT---GTACAAGTTGCTGAAAAGCCAGCAGCTGAG 488
Db	
482	AGAAGAGCACTGCCAGTATTTCTGTACCAAGATCTCTGGGGGCTCAAGTACATCCACTC 541
Db	
489	CAATGACCAATATCTGTACTTCTCTACCAAGATCTCTCGGGGCTCAAGTACATCCACTC 548
Db	
542	GGCGAACTGTATCCACCGCAGCTGGAAGCGAGCAACCTGCTGCTGAAGCCCAACTGCCGA 601
Db	
549	CGCCACGTGCTCCACGAGATCTAAGCCCTCAACCTGCTCAGCAACACCACTTGCGGA 608
Db	
602	CCTCAAGATCTCGAATTGGGGTGGCGGG-----CCGTGCTCGGAGAGCGA 649
Db	
609	CCTTAAGATTGTGATTTTCGGCCTGGCCCGGATTCGGATCTCTGAGCATGACCACACCGG 668
Db	
650	CATGATGACGAGTACTGTGTACCCGGTGGTACCGGCGCGGAGCTGCTCTCAACTC 709
Db	
669	CTTCTTGACGGATATGTGGCTACGGCTGGTACCGGGCCCGAGATCATGCTGAATC 728
Db	
710	CACCGACTACTCTCGCGCCCATCGACGCTCTGGTCCGTCCGTGCTATTTCAATGAGCTCAT 769
Db	
729	CAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGTGCAATCTGGCTGAGATGCT 788
Db	
770	CAACCGCCAGCGCTCTTTCCCGCGGACGGACCAATGACACAGATGCGCTCATACCGGA 829
Db	
789	CTCTAAACCGGCCCATCTTCTCGTGGCAAGCACTACTCGATCAGCTCAACCAATTTCTGGG 848
Db	
830	GGTGATCGGACCGCGAGCGACGAGCTGGGGTTTCATACGGAACGAGAGACCGGAGGA 889
Db	
849	CATCTGGGCTCCCCATCCCAGAGGACCTGAAATTTGTTATCATCAACATGAAGGCCCGAAA 908
Db	
890	GTACATGAGGCACCTGCGCGAGTACCCCGCCCGGACGTTCCGAGCATGTTTCCCGGGGT 949
Db	
909	CTACCTACAGTCTCTGCCCCTCAAGACCAAGTGGCTTGGGCCAAGCTTTTCCCAGATC 968
Db	
950	GCAGCCCGCGCTCGACCTCATTCGAGAGGATGCTCACTTCAAACCGCTGCGAGAGAT 1009
Db	
969	AGACTCCAAAGCCCTTGACCTGTCTGGACCGGATGTTAAACCTTTAAACCCCAATTAACGGAT 1028
Db	
1010	CACAGTTTGAAGGCGCTCCGATCATCTTACCTAGAGAGATTGCAGACATCCCGATGA 1069
Db	
1029	CACAGTGGAGGAGCGCTGGCTCACCCTTACCTGGAGAGATGACTATGACCCGACGGATGA 1088
Db	
1070	GCCCATCTGCTGGAGCCCTTCTCTTCGACTTCGAGCAGAGGCTCTAAACGAGGACCA 1129
Qy	

Db 1089 GCCAGTGGCCGAGGAGCCCTTACCTTCGCCATGGAGCTGGATGACCTACCTAAGGCG 1148
 Qy 1130 AATGAGCAGCTGATCTTCAACGA 1153
 Db 1149 GCTGAAGGAGCTCATCTTCCAGA 1172

RESULT 6

```

US-09-417-197-38
; Sequence 38, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-Erk1 fusion construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (1893)
US-09-417-197-38

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Db 1413 CAAGGGCTATACCAAGTCCATCAGCATCTGGTCTGTGGGCTGCATTTCTGGCTGAGATGCT 1472
QY 770 CAACCGCCAGCCGCTCTTCCCGGCGAGGACACATGACAGATGGCGCTCATCACCGA 829
Db 1473 CTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACACATTTCTGGG 1532
QY 830 GGTGATCGGAGCCCGGACGAGCAGAGCTGGGGTTCAATCGGAAACGAGACCGGAGAA 889
Db 1533 CATCTCTGGGCTCCCATCTCCAGGAGGACCTGAATTTGATCATCAATGAAGGCCCGAAA 1592
QY 890 GTACATGAGCACCTGCGCAGTACCGCGCCGAGGCTTGGCGAGCATGTTCCCGGGGT 949
Db 1593 CTACCTACAGTCTTGGCTTCCAGACCAAGTGGCTTGGGCCCAAGCTTTTCCCAAGTC 1652
QY 950 GCAGCCCGCCGCTCGACCTCATCGAGAGATGCTCACCTTCAACCCGCTGCAGAGAAAT 1009
Db 1653 AGACTCCAAAGCCCTTGACCTGTGACCGGATGTTAACTTTAAACCCCAATAACGGAT 1712
QY 1010 CACAGTTGAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGCAACATGCCGATGA 1069
Db 1713 CACAGTGGAGAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACGATGA 1772
QY 1070 GCCCATCTGCTGGAGCCCTTCTCTTCCGACTTCGAGCAGAGGCTTAAACGAGACCA 1129
Db 1773 GCCAGTGGCGAGGAGCCCTTCACTTGGCCATGGAGTGGATGACCTACCTTAAGGAGCG 1832
QY 1130 AATGAAGCAGCTGATCTTCAACGA 1153
Db 1833 GCTGAAGGAGCTCATCTTCCAGGA 1856
RESULT 7
US-09-417-197-56
; Sequence 56, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mERK1-F64L-S65T-GFP fusion
; NAME/KEY: CDS
; LOCATION: (1)..(1872)
US-09-417-197-56
Query Match 23.9%; Score 334; DB 3; Length 1875;
Best Local Similarity 61.1%; Pred. No. 5.7e-64;
Matches 601; Conservative 0; Mismatches 365; Indels 18; Gaps 3;
QY 182 CGAGCGCCCATCATGCCCATTTGGCGCGCTACGGGATGCTGTCTCGTCCGTGATGAA 241
Db 126 CTACACGCACTGCAGTACATCGCGGAGCGGTACGGCATGTGTCAGCTCATGATGA 185
QY 242 CTTTGTAGACAGGAGAGTGTGGCGATAAAGAGATCGCCACCGCTTCAACACACAT 301
Db 186 CCAGTGTGCGCAACACAGAGTGGCCATCAAGAGAT---CAGCCCTTTTGGAGATCAAC 242
QY 302 GGACGCCAAGCGCACGCTCCGGAGATCAAGCTCTTCAGGACCTCGACACGAGAACAT 361
Db 243 CTACTGTGACGCGCACGCTGAGGAGATCCAGATCTTGTGCGATTCGGCATGAGAATGT 302
QY 362 CATAGGCATCAGGAGTGTGATCCCGCGCGATCCCTCAGGCGCTTCAACAGCTCTACAT 421

Db 303 TATAGGCATCCGAGACATCTCTCAGAGCGCCACCTCGAAGCCATGAGAGATGTTTACAT 362
QY 422 CGCCACGGAGCTCATGAGCACCGAGCTCCATCACATCATCTCCCTCCAAACAAGAACTGTC 481
Db 363 TGTTCAGGACCTCATGAGAGACAGACT---GTACAACTGCTTAAAGCCAGCAGCTGAG 419
QY 482 AGAAGAGCACTGCCAGTATTTCTGTACAGATCTTGGGGGGCTCAAGTATCATCCTACTC 541
Db 420 CAATGACCACATCTGCTACTTCTCTACAGATCTCCGGGGCTCAAGTATATACACTC 479
QY 542 GCGCAACTGTATCCACCGGACCTCAAGCGAGCAACCTGCTGCTGACGCCCACTGCCA 601
Db 480 AGCCAAATGTGCTGCAACCGGACCTTGAAGCTTTCAAATCTGCTTATCAACACCACTGCCA 539
QY 602 CCTCAAGATCTCGCACTTCTGGGCTGGCGCG-----CGTCTGTCGAGAGCGA 649
Db 540 CTTTAAAGATCTGTGATTTTGGCTTGGCCCTGGCCCGGATTTGCTGACCTGAGCAGCACCACTGG 599
QY 650 CATGATGACGAGTACGTGGTCAACCCGGTGTGACCGCGCGGAGCTGCTCTCAACTC 709
Db 600 CTTTCTGACGAGTATGTGGCCACACGCTGTGTACCGAGCCCGAGAGATCATGCTTAAATTC 659
QY 710 CACGCACTACTCCGGCGGCATCGAGCTGTGGTCCGCTCGCTGCTCATGAGCTCAT 769
Db 660 CAAGGGCTACACAAATCCATCGACATCTGGTCTGTGGGCTGCAATTTCTGGCTGAGATGCT 719
QY 770 CAACCGCCAGCGCTCTTCCCGCGAGGAGCACATGACACAGATGCGCTCATCACCGA 829
Db 720 CTCCAACCGGCCCATCTTCCCGGCAAGCATCTACCTGGACAGCTCAACCATTTCTAGG 779
QY 830 GGTGATCGGAGACGCGACGAGCTGGGGTTTATACGAAACGAGGACGCGAGGAA 889
Db 780 TATCTTGGGTTCCCATCCAGAGGAGCTTAAATTCATCATTAACATGAAGGCCCGAAA 839
QY 890 GTACATGAGGACCTGCGCGAGTACCCGCGCGAGCTTTCGCGAGCATGTTCCCGGGGT 949
Db 840 CTACCTGAGTCTCTGCGCTCGAAACCAAGTGGCTTGGGCCAAGCTCTTTCTTAAATC 899
QY 950 CGAGCCCGCGCTCGACCTCATCGAGAGATGCTCACTTCAACCCGCTCGAGAGAT 1009
Db 900 TGACTCCAAAGCTCTTGACCTGCTGGAACGGATGTTAACTTCAACCCCAACAGCGCAT 959
QY 1010 CACAGTTGAGGAGCGCTCGATCATCTTACAGAGATTTGACGAGCATCGCGATGA 1069
Db 960 CACAGTAGAGGAAAGCGCTGGCTCACCTTACCTGGAACAGTACTACGATCCGACAGATGA 1019
QY 1070 GCCCATCTGCTGGAGCCCTTCTCTTCCGACTTCGAGCAGAGGCTTAAACGAGACCA 1129
Db 1020 GCCAGTGGCGGAGGAGCATTCACCTTCGACATGGAGTGGATGACCTCCCAAGGAGCG 1079
QY 1130 AATGAAGCAGCTGATCTTCAACGA 1153
Db 1080 GCTGAAGGAGTGTGATCTTCCAGGA 1103

RESULT 8

US-09-828-313-8/c
; Sequence 8, Application US/09828313
; Patent No. 6867351
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-8

Query Match 22.9%; Score 319.8; DB 3; Length 953;
Best Local Similarity 64.7%; Pred. No. 6.3e-61;
Matches 491; Conservative 0; Mismatches 267; Indels 1; Gaps 1;

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QY 405 TTCAACGAGCTCTACATGCGCAGGAGCTCATGACACCGACTCCATCATCATCTCCG 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 TTCAACGAGCTCTACATGCGCAGGAGCTCATGACACCGACTCCATCATCATCTCCG 885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 465 TCCAACCAAGAACTGTCCAGAGAGCACTGCCAGTATTTCTGTACAGATCTCTGCGGGG 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 TCAATCAAGCTCTCACAGAGACCACTGTCAATTTCTGTATCAATCTTGGGGG 825
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 CTCAGGTATCATCTCGGCGAAGCTGATCCACCGCACTGAAAGCGGAGCAACCTGCTG 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 TTGAAGTATCATCTCGGCGAAGCTGATCCACCGCACTGAAAGCGGAGCAACCTTCTC 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 585 CTGAAGCCCACTGCGCACTCAAGATCTGCGACTTGGGCTGGGGCGGCGTCTCGGAG 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 GTCAATGCCAATTTGCCATTTGAAATCGCAGATTTTGGCTTGGCAGCGCACTCTCTGAA 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 645 AGCGCATGATGACGAGTACGTGGTCAACCGGTGTACCGCGCGCGGAGCTGTGCTC 704
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 ACGGATTTCACTGATGATGTTGTAACGAGGTGTACAGACTCAGAGCTGCTCTCTG 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 705 AACTCCACCGACTCTCCGCGGCATCGAGCTGTGGTCCGTCCGCTGCATCTTATGGAG 764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 AATTGTTACGATACACTGCGACTTATGACATTTGGTCTGTGGGTGCACTTCTATGGAG 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 765 CTATCAACCGCAGCGCTCTCCCGGAGGAGCAATGACACGATGCGCCTCATC 824
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TTGCTTAAACCGATCTGCGTTGTTCCCTGGGAGAGACTATGTGCATCAGCTCCGCTAAAT 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 825 ACCGAGTGTATCGGAGCGCGCAGCGAGCTGGGGTTTCATACGGAACGAGGACGG 884
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 ACGAAGTATCGAAGTCTCTGAGATAGGATCTTGGGTTTGGAGCGGACATGCT 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 885 AGGAAGTATAGGAGCACTCGCGCAGTACCCGCGCGGAGCTTCCGCGAGCATGTTCCCG 944
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 AGCGGTATATCAAGCACTGCTCGACAGTGGCTTATTCCTTAAACCCAGAGTTTCA 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 945 CGGGTGCAGCCCGCGGCTCGACCTCATCGAGAGATGCTCACTTCAACCGCTGCAG 1004
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 GCGATTAATCGTTCTGCTCTGTATCTTGTGAAAGATGCTGTGCTTTGATCCAGCGAA 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1005 AGAATCACAGTTGAGGAGCGCTCGATCATCTTACCT-AGAGAGATTGACACCATCGC 1063
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 AGAATCACAGTGAAGTCTGCTTGGCGACCTTATTAAGTTCATTCATGACATCAA 285
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QY 1064 CGATGAGCCCATCTGCTGAGGCGCTTCTCTTTCGACTTCGAGCAGAGAGCTCTAAACGA 1123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 CGATGAGCTGGCTCGGTATCTCCCTTCGAGTTGGCTTCGAGGAGCCCTCTATCTCGA 225
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QY 1124 GGAACCAATGAAGAGCTGATCTTCAACAGAGCGATCGA 1162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 GGAACCTATCAGGATCTCTATTTGGAGGAGGCTCTGGA 186
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RESULT 9

US-08-176-620A-1
; Sequence 1, Application US/08176620A
; Patent No. 5595904
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G.
; APPLICANT: Cobb, Melanie H.
; APPLICANT: Yancopoulos, George D.

; APPLICANT: Nye, Steven
; APPLICANT: Panayotatos, Nikos
; TITLE OF INVENTION: A Family of Map2 Protein Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,620A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1747 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
; US-08-176-620A-1

Query Match 22.8%; Score 318; DB 2; Length 1747;

Best Local Similarity 60.1%; Pred. No. 1.9e-60;

Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;

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QY 182 CCAGCGCCCATCATGCCATTTGGCGCGCGCTACGGGATGCTGTCTCGTGTGATGA 241
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Db 81 CTACACGCGAGCTGCAGTACATCGCGAGGCGGTACGGCTCAGCTCAGCATATGA 140
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QY 242 CTTTGAGACGAGGAGATGTTGGCGATAAAGAGATCGCCAGCGCTTCAACACGACAT 301
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Db 141 CCACGTGCGCAAGACCGAGATGGCTATCAAGAAGAT---CAGCCCTTTCGAGCATCAAAC 197
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QY 302 GGAAGCCAAAGCGCAGCTCCGCGAGATCAAGCTCTCAGGCACCTCGACCAAGACAT 361
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Db 198 CTACTGTGAGCGACCTCGAGAGAAATCCAGATCTTGTCTGGATTCGCCCATGAGATGT 257
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QY 362 CATAGGCATCAGGATGTGATCCCGCGCGCGATCCCTCAGGCGTTCAAAGCGCTTACAT 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CATAGGCATCCGAGACATCTTCAGAGCACCCCTCGAAGCCATGAGAGATGTTTACAT 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 422 CGCCACGAGCTCATGGACACCGACCTCCATCATCATCTCCGCTCCAAACCAAGACTGTC 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 TGTTCAGGACCTCATGGAGCGGACCT---GTACAAAGCTGCTAAAGAGCCAGAGCTGAG 374
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QY 482 AGAAGAGCACTGCCAGTATTTCTGTACAGATCTTCGCGGGCTCAAGTACATCCACTC 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 CAATGACCAATCTGCTACTTCTTACCAGATCTCCCGGGCTCAAGTACATCACTC 434
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 542 GCGAAGCTGATCCACCGCGACCTGAAGCGCGAGCAACCTGCTGCTGNAAGCCCACTGCGA 601
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Db 435 GGCCATGTGCTGCACCGGAGCTGAAGCCCTCAATCTGCTTATCAACACCACTGCGA 494
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QY 602 CCTCAAGATCTGCGACTTCGGGCTGGCGGG-----CCGTCGTCGAGAGCGA 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,887
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,544
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-049
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1747 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1095
 US-08-458-887-1

Query Match 22.8%; Score 318; DB 2; Length 1747;
 Best Local Similarity 60.1%; Pred. No. 1.9e-60;
 Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;

182 CCAGCGCCCATCATGCCATTTGGCGCGCTACGGGATCGTCTGCTCCGATGAA 241
 81 CTACAGCGACTGCAGTACATCGCGGCGGTACGGATGCTCAGCTCAGCATGA 140
 242 CTTTGAGACGAGGAGATGTTGGCGATTAAGAAGATCGCCAAACGCGTTCAACACGACAT 301
 141 CCACGTGCGCAAGACAGAGTGGCTATCAAGAAGAT---CAGCCCTTCGAGCATCAAAAC 197
 302 GGACGCCACGCGACCGCTCGGGAGATCAAGCTCCTCAGGCACCTCGACACGAGACAT 361
 198 CTACTGTTCAGCGACCGCTGAGAGAAATCCAGATCTTGTGCGGATTCGCGCATGAGATGT 257
 362 CATAGGCATCAGGATGTGATCCGCGCGGATCCCTCAGGCGGTTCACGACGTCTACAT 421
 258 CATAGGCATCCGAGACATCTCTAGAGACCCACCTCGGAAGCCATGAGATGTTTACAT 317
 422 CGCCACGAGCTCATGGACACCGACCTCCATCATCATCCGCTCCAAACCAAGATGTGC 481
 318 TGTTTCAGGACCTCATGGAGACGACCT---GTACAAGCTGCTAAAGAGCCAGCAGCTGAG 374
 482 AGAAGACACTGCCAGTATTTCTGTACAGATCTCGGGGCTCAAGTACATCCACTC 541
 375 CAATGACCATCTGTCTACTTCTCTACAGATCTCTCGGGGCTCAAGTACATCACTC 434
 542 GGGCAACGCTGATCCACCGCGACCTGAAAGCGAGCAACCTGCTGCTGAACGCCAACTGCGCA 601
 435 GGCATATGCTGCAACCGGACCTGAAGCCCTCCATCTGCTTATCAACACCACTTGGCA 494
 602 CTTCAAGATCTCGGACTTCGGGTGGCGCG-----CCGTGTCGAGAGCGCA 649

Db 495 CTTAAGATCTGTGATTTTGGCTTGGCCGATTTGCTGACCTGAGCAGCAGCACACTGG 554
 Qy 650 CATGATGACGGAGTACGTGCTCACCCTGTTGGTACCGCGCGCGGAGCTGCTCTCAACTC 709
 Db 555 CTTTCTGACCGAGTATGTGGCCACACGCTGTGACGAGCCCGCAGAGATCATGCTTAACTC 614
 Qy 710 CACGACTACTCCGCGCCATGAGCGTCTGFTCGTGGCTGATCTTTCAATGAGAGTCAAT 769
 Db 615 CAAAGGGCTACACAAATCCATTGACATCTGGTCTGTGGCTGCAATCTGGCTGAGATGCT 674
 Qy 770 CAAACCGCAGCGCTCTTCCCGGCGAGGACACATGACACCATGCGCTCATCACCGA 829
 Db 675 CTCCTAACCGGCTATCTTCCCGGCGAAGCAGCTTACCTGGACCAAGCTCAACCATTTCTAGG 734
 Qy 830 GGTGATCGGAGCGCGACGAGCGAGCTGGGGTTTCATACGGAACGAGGAGCGCGAGAA 889
 Db 735 TATACTGGGTTCCCATCCCAAGAGGACCTAAATTGTATTAATCAATGAAGGCCGAAA 794
 Qy 890 GTACATGAGGCACTCGCGCGAGTACCCGCGCGAGCGTTCGCGAGCATGTTCCCGGGGT 949
 Db 795 CTACCTACAGTCTCTGCTCCCTCTAAACCAAGGTGGCTTTGGGCAAGCTTTTCCCAATC 854
 Qy 950 GCAGCGCGCGCTCGACCTCATCGAGAGATGCTCAGCTTCAACCCGCTCGAGAGAT 1009
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 Qy 1010 CACAGTTGAGGAGCGCTCGATCATCTTACCTAGAGAGATGTCAGCATCGCGATGA 1069
 Db 915 CACAGTAGAGAGACACTGGCTCACCCTTACCTGGAACAGTACTATGATCCGACAGATGA 974
 Qy 1070 GCCCATCTGCTGGAGCCCTTCTCTCGACTTCGAGCAGAGAGGCTTAAACGAGAGACA 1129
 Db 975 ACCAGTGGCTGAGGAGCCATTCACTTTGACATGAGCTGGATGATCTCCCAAGAGCG 1034
 Qy 1130 AATGAAGAGCTGATCTTCAACGA 1153
 Db 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058

RESULT 13
 US-08-932-787B-1
 ; Sequence 1, Application US/08932787B
 ; Patent No. 6277963
 ; GENERAL INFORMATION:
 ; APPLICANT: Boulton et al.
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
 ; TITLE OF INVENTION: KINASES
 ; FILE REFERENCE: REG 430-A-1
 ; CURRENT APPLICATION NUMBER: US/08/932,787B
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 08/469,547
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: 08/178,488
 ; PRIOR FILING DATE: 1994-01-07
 ; PRIOR APPLICATION NUMBER: 07/701,544
 ; PRIOR FILING DATE: 1991-05-16
 ; PRIOR APPLICATION NUMBER: 07/532,004
 ; PRIOR FILING DATE: 1990-06-01
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1747
 ; TYPE: DNA
 ; ORGANISM: RAT
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1095)
 ; OTHER INFORMATION: ERK1 cDNA
 US-08-932-787B-1

Query Match 22.8%; Score 318; DB 3; Length 1747;
 Best Local Similarity 60.1%; Pred. No. 1.9e-60;
 Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;


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QY 182 CAGCGCCCATCATGCGCCATTGGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAA 241
Db 81 CTACACGAGCTCAGTATACATCGCGAGCGCGGTACGGCATGCTCAGCTCAGCATATGA 140
QY 242 CTTTGTAGAGAGGAGATGCTGGCGATAAAGAGATCGCCACGCGTTCAACAACGACAT 301
Db 141 CACGCTGCGCAAGACAGAGTGGCTATCAAGAAGAT---CAGCCCTTTCAGCATCAAC 197
QY 302 GGAAGCAAGCGCAGCTCCGGGAGATCAAGCTCCTCAGSCACCTCGACACGAGAACAT 361
Db 198 CTACTGTGCGCAGCAGTGGAGAAATCCAGATCTTGTCTCGGATTCGGCCATGAGAATGT 257
QY 362 CATAGGATCAGGATGTGATCCCGCGCGGATCCCTCAGGCGTTCAAAGAGCTTACAT 421
Db 258 CATAGGATCCGAGATCTCTCAGAGCACCCACCTCGAAGCCATGAGAGATGTTTACAT 317
QY 422 CGCCACGAGCTCATGAGACCGACCTCCATCATCATCCGCTCCAAACCAAGAACTGTC 481
Db 318 TGTTACGAGCTCATGAGACCGACCT---GTAAAGCTCTAAAGAGCCAGCGTGGAG 374
QY 482 AGAAGAGCATGCGCAGTATTTCTGTACAGATCTCTCGGGGCTCAAAGTACATCCACTC 541
Db 375 CAATGACCATCTGCTACTTCTCTACAGATCTCTCGGGGCTCAAAGTACATCCACTC 434
QY 542 GCGGAACTGATCCACCGGACCTGAAAGCGAGAACCTGCTGCTGAAACCGCAACTGCGGA 601
Db 435 GCGCAATGTGCTGACCGGAGCCTGAAAGCCTCCAATCTGCTTATCAACACCACTCGGA 494
QY 602 CCTCAGATCTGCGACTTCGGGTGGCGG-----CCGCTCGTGGAGGCGGA 649
Db 495 CCTTAAGATCTGATTTTGGCTTGGCCGATGCTGACCTGAGACGACCACTACTGG 554
QY 650 CATGATGACGAGTACGTGGTCAACCGGCTGTTACCGCGCGCGAGCTGCTGCTCAACTC 709
Db 555 CTTTCTGACCGAGTATGTGGCCACACGCTGGTACCGAGCCCGAGAGATCATGCTTAATC 614
QY 710 CACCGACTACTCCCGCGCCATCGACGCTGGTCCGTCGGTGCATCTTCAATGAGGCTCAT 769
Db 615 CAAGGGCTACACCAAAATCCATGACATCTGCTGTGGGCTGCATCTGGCTGAGATGCT 674
QY 770 CAACCGCCAGCGCTCTTCCCGCGAGGACCATGACACGATGCGCTCATCACCGA 829
Db 675 CTCACCGGCTATCTTCCCGGCAAGCACTACCTGGAACGATCAACCACTTCTAGG 734
QY 830 GGTGATCGGACCGCGACGACGAGCTGGGGTTATACGGAACGAGGACGCGAGAA 889
Db 735 TATACTGGGTTCCCATCCCAAGAGGACCTAAATTTGATCATTTAAATGAAGGCCGAAA 794
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QY 950 GCGCGCGCGCGCTCGACCTCATCGAGAGATGCTCACTTCAACCGCTGAGAGAT 1009
Db 855 TGACTCCAAAGCTCTTGACCTGCTGGAACCGGATGTTAAACCTTTAAACCAACGAGCAT 914
QY 1010 CACAGTTGAGGAGCGCTCGCATCATCTTACCTTAGAGAGATGTCACCAATCGCCGATGA 1069
Db 915 CACAGTAGAGAGAGCATGCTCACCCTTACCTGGAACAGTACTATGATCGGACAGATGA 974
QY 1070 GCCCATCTGCTGGAGCGCTTCTCTTTCGATCTTCGAGCAGAGGCTCTAAACGAGGACCA 1129
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QY 1130 AATGAACGAGTATCTTCAAGA 1153
Db 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058
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RESULT 14

US-08-932-012C-1

; Sequence 1, Application US/08932012C

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; Patent No. 6297035
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-Y-1
; CURRENT APPLICATION NUMBER: US/08/932,012C
; CURRENT FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 08/462,874
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1095)
; OTHER INFORMATION: ERKL cDNA
; US-08-932-012C-1
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Query Match 22.8%; Score 318; DB 3; Length 1747;

Best Local Similarity 60.1%; Pred. No. 1.9e-60;

Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;

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QY 182 CAGCGCCCATCATGCGCCATTGGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAA 241
Db 81 CTACACGAGCTCAGTATACATCGCGAGCGCGGTACGGCATGCTCAGCTCAGCATATGA 140
QY 242 CTTTGTAGAGAGGAGATGCTGGCGATAAAGAGATCGCCACGCGTTCAACAACGACAT 301
Db 141 CACGCTGCGCAAGACAGAGTGGCTATCAAGAAGAT---CAGCCCTTTCAGCATCAAC 197
QY 302 GGAAGCAAGCGCAGCTCCGGGAGATCAAGCTCCTCAGSCACCTCGACACGAGAACAT 361
Db 198 CTACTGTGCGCAGCAGTGGAGAAATCCAGATCTTGTCTCGGATTCGGCCATGAGAATGT 257
QY 362 CATAGGATCAGGATGTGATCCCGCGCGGATCCCTCAGGCGTTCAAAGAGCTTACAT 421
Db 258 CATAGGATCCGAGATCTCTCAGAGCACCCACCTCGAAGCCATGAGAGATGTTTACAT 317
QY 422 CGCCACGAGCTCATGAGACCGACCTCCATCATCATCCGCTCCAAACCAAGAACTGTC 481
Db 318 TGTTACGAGCTCATGAGACCGACCT---GTAAAGCTCTAAAGAGCCAGCGTGGAG 374
QY 482 AGAAGAGCATGCGCAGTATTTCTGTACAGATCTCTCGGGGCTCAAAGTACATCCACTC 541
Db 375 CAATGACCATCTGCTACTTCTCTACAGATCTCTCGGGGCTCAAAGTACATCCACTC 434
QY 542 GCGGAACTGATCCACCGGACCTGAAAGCGAGAACCTGCTGCTGAAACCGCAACTGCGGA 601
Db 435 GCGCAATGTGCTGACCGGAGCCTGAAAGCCTCCAATCTGCTTATCAACACCACTCGGA 494
QY 602 CCTCAGATCTGCGACTTCGGGTGGCGG-----CCGCTCGTGGAGGCGGA 649
Db 495 CCTTAAGATCTGATTTTGGCTTGGCCGATGCTGACCTGAGACGACCACTACTGG 554
QY 650 CATGATGACGAGTACGTGGTCAACCGGCTGTTACCGCGCGCGAGCTGCTGCTCAACTC 709
Db 555 CTTTCTGACCGAGTATGTGGCCACACGCTGGTACCGAGCCCGAGAGATCATGCTTAATC 614
QY 710 CACCGACTACTCCCGCGCCATCGACGCTGGTCCGTCGGTGCATCTTCAATGAGGCTCAT 769
Db 615 CAAGGGCTACACCAAAATCCATGACATCTGCTGTGGGCTGCATCTGGCTGAGATGCT 674
QY 770 CAACCGCCAGCGCTCTTCCCGCGAGGACCATGACACGATGCGCTCATCACCGA 829
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Db 675 CTCACACCGGCTATCTTCCCGGCAAGCACTACCTGGACCAGCTCAACCAATTTCTAGG 734
Qy 830 GGTGATCGGGAGCGCCGACGAGCAGCAGCTGGGGTTTCATACGGAACGAGGACGCGAGAA 889
Db 735 TATACCTGGGTTCCCATCCCAAGAGACCTAAATTTGTATCATTAACATGAGGCCCGAAA 794
Qy 890 GTACATGAGGCACCTGCCGAGTACCCGCGCGGACGTTTCGGAGCATGTTCCCGGGGT 949
Db 795 CTACCTACAGTCTCTGCCCTCTAAACCAAGGTGGCTTGGGCCAAGCTTTTCCCAAATC 854
Qy 950 GAGCCCGCGCGCTCGACTCATCGAGAGGATGCTCACTTCAACCCGCTGAGAGAAAT 1009
Db 855 TGACTCCAAAGCTCTTGACCTGCTGGACCGGATGTTAACTTTAAACCCAAACAAAGCGCAT 914
Qy 1010 CACAGTTGAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGCAGACATGCCGATGA 1069
Db 915 CACAGTAGAGGAAGCACTGGCTCACCTTTACCTTGGAAACAGTACTATGATCCGACATGA 974
Qy 1070 GCCCATCTGCTGGAGCCCTTCTCTTCGACTTCGAGCAGAAGGCTCTAAACGAGGACCA 1129
Db 975 ACCAGTGGCTGAGGAGCCATTACCTTTGACATGGAGCTGGATGATCTCCCCAAGGAGCG 1034
Qy 1130 AATGAAGCAGCTGATCTTCAACGA 1153
Db 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058

RESULT 15

US-08-888-818C-1
; Sequence 1, Application US/08888818C
; Patent No. 6303358
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-V-1
; CURRENT APPLICATION NUMBER: US/08/888,818C
; CURRENT FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: 08/478,985
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1095)
; OTHER INFORMATION: BRK1 cDNA
US-08-888-818C-1

Query Match 22.8%; Score 318; DB 3; Length 1747;
Best Local Similarity 60.1%; Pred. No. 1.9e-60;
Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;
Qy 182 CCAGCGCCCATCATGCCCCATTTGGCGCGCGCTACGGGATCGTCTGCTCCGATGATGA 241
Db 81 CTACAGCAGCTGCAGTACATCGCGGAGGCGGTACGGCAGTGTGCTCAGCTCAGCATATGA 140
Qy 242 CTTTGTAGACGAGGAGATGTTGGCGATTAAGAGATGGCCACCGCGTTCAACCAACCAT 301
Db 141 CCACGTGGCGAAGACCAAGTGGCTATCAAGAAGAT---CAGCCCTTTCAGCATCAAAC 197
Qy 302 GGAGGCCAGCGCAGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCCAGGAAAT 361
Db 198 CTACTGTACGCGCACGCTGAGAGAAATCCAGATCTTGTCTCGGATTCGCGCATGAGATGT 257

Qy 362 CATAGGCACTAGGGATGTGATCCCGCGCGCATCCCTCAGGCGTTTCAACGACGTCTACAT 421
Db 258 CATAGGCACTCGAGACATCCCTCAGAGCACCCACCCCTGGAAGCCATGAGAGATGTTTACAT 317
Qy 422 CGCCACGAGGCTCATGGACACGAGCTCATCATCATCATCCGCTCAACCAAGAACTGTC 481
Db 318 TGTTCAGGACCTCATGGAGACGACCT---GTACAAGCTGTAAAGAGCCAGCAGCTGAG 374
Qy 482 AGAAGACACTGCGAGTATTTCTGTACAGATCTCGGGGGGCTCAAGTATCATCCACTC 541
Db 375 CAATGACCACTCTGCTACTTCTCTACAGATCTCTCGGGGCTCAGTATCATCATCTC 434
Qy 542 GCGCAACGATGATCCACCGGACCTGAAGCCGAGCAACTGCTGTGAACGCCAACTGCGA 601
Db 435 GCGCAATGTGCTGCACCGGGACCTGAAGCCCTCCAATCTGCTTATCAACACCACTGCCA 494
Qy 602 CCTAAGATCTCGAGACTTTCGGGCTGGCGGG-----CGTCTCGGAGAGCA 649
Db 495 CTTAAGATCTGTGATTTTGGCTTTGCCCGGATTGCTGACCTGAGCAGACCACTGG 554
Qy 650 CATGATGACGAGTACGTGGTCACCCGCTGGTACCGCGCGCGGAGCTGCTCTCAACTC 709
Db 555 CTTTCTGACCGGATATGTGGCCACAGCTGTGTACCGAGCCCGAGAGATCATGCTTAACTC 614
Qy 710 CACCGACTACTCCGCGCCCATCGAGCTCTGGTTCGTCGCTGTCATCTTTCATGGAGCTCAT 769
Db 615 CAAGGGCTACACCAAAATCCATTGACATCTGGTCTCTGGGCTGCAATCTTGGCTGAGATGCT 674
Qy 770 CAACCGCAGCGCTCTTCCCGGAGGAGCACATGACACAGATGGCGCTCATCACCA 829
Db 675 CTCCAACCGGCTATCTTCCCGGCAAGCACTACCTGGACCAAGCTCAACCAATTTCTAGG 734
Qy 830 GGTGATCGGACGCGAGCAGAGCTGGGTTTCATACGGAACGAGAGCGCGAGAA 889
Db 735 TATACCTGGGTTCCCCATCCAAAGAGACCTAAATTTGTATCATTAACATGAAGGCCCGAAA 794
Qy 890 GTACATGAGGCACCTTGGCGCAGTACCCGCGCGGACGTTTCGCGAGCATGTTCCCGGGT 949
Db 795 CTACCTACAGTCTCTGCGCTCTAAACCAAGGTGGCTTGGGCCAAGCTTTTCCCAAATC 854
Qy 950 GAGCCCGCGCGCTCGACCTCATCGAGAGGATGCTCAGCTTCAACCCGCTGAGAGAAAT 1009
Db 855 TGACTCCAAAGCTCTTGGACCTGCTGGACCGGATGTTAACTTTAAACCCAAACAAAGCGCAT 914
Qy 1010 CACAGTTGAGGAGCGCTCGATCATCTTACCTAGAGAGATTGACAGCATCGCCGATGA 1069
Db 915 CACAGTAGAGGAGCACTGGCTCACCTTACCTGGAACAGTACTATGATCCGACATGA 974
Qy 1070 GCCCATCTGCTGGAGCCCTTCTCTTCGACTTCGAGCAGAAGGCTCTTAAACGAGGACCA 1129
Db 975 ACCAGTGGCTGAGGAGCCATTCACTTTGACATGGAGCTGGATGATCTCCCCAAGGAGCG 1034
Qy 1130 AATGAAGCAGCTGATCTTCAACGA 1153
Db 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058

Search completed: December 29, 2005, 07:49:10
Job time : 206 secs

D_b 301 TGGACGCCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCACGAGACA 360


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Db      853 CATCTCCAGCGCACTCGTGGCGCCGACCGAGCGTCTGGTCCGCGAGCTCATCTTCATGC 912
Qy      593 CAACTGCGACCTCAAGATCTGCGACTTCGGGGCTGGCGCGCGCTCGTGGAGAGCGACAT 652
Db      913 CGCCCATCAACCGCGGTCTCTCCCGGGGAGGACACATGACACAGATGCGGCTAT 972
Qy      653 GATGACGAGTGTGTTGATCAACCGGTGTGTAACCGGC-----GCCGAGCTGCTGC 702
Db      973 GCACGGGGTGTCTGTCAACCGCGCGGACAGACGACCCCGATTCACCGCGGACCGAGGAC 1032
Qy      703 TCAACTCCACCGCACTACTCGCGCCATCGAGCTCTGGTTCGGTGGCTGCATCTTCATGG 762
Db      1033 GCCAGAGGTACATGAGGACCTGCGGAGTTCCTTCGCGGCTCTTCACGAGGCGATG 1092
Qy      763 AGCTCATCAACCGCGCGCTCTTCGCGGCA--GGGACCAATGACACAGATGCGCT 820
Db      1093 CCCAAGGTGACCGCGCGCTGCGACCTCATCGAGAGGATATTCACCTGATCGGCT 1152
Qy      821 CATACCGAGGTGATCGGAGCGCGGACGAGCGAGCTGGGGTTCATAGGAGCGAGGA 880
Db      1153 TATCAGCGATGTATCGGCAACCGCGGACGACCTGGGTATTAATCCGGAACGAGGA 1212
Qy      881 CGCGAGGAGTACATGAGG--CACTGCGGAGTACCGCGCGGAGCTTCGCGAGCATGT 939
Db      1213 CGCAGGAGTACATGAGGCGACCTGCGGAGTTCCTTCGCGGCTCTTCGCGGAGAT 1272
Qy      940 TCCCGGGGTGACGCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCGC 999
Db      1273 TCCCAAGGTGACGCGCGCGCTGACCTCATCGAGAGGATGCTCACCTTCAACCCGC 1332
Qy      1000 TGACAGATACAGTTGAGGAGCGCTGATCATCTTACCTAGAGAGATTGACAGACA 1059
Db      1333 TGACAGAGTACAGTTGAGAGCGCTGAGGACCACTACCTAGAGCGGCTTACGAGC 1392
Qy      1060 TCGCGATGAGCCATCTGCTGAGCGCTCTCTTCGACTTCGAGCGAGGCTCTAA 1119
Db      1393 TCGCGAGGAGCCATCTGACGAGCCCTCTCTTCGACTTCGAGCGAGCCACTGA 1452
Qy      1120 ACCAGACCAATGAAGCAGCTCATCTTCAAGAGCGATCGAGATGAACCCCAACATCC 1179
Db      1453 CGGAGACCAAGATGAGCAGCTCATCTTCAAGAGCCCTGGAGTTGAAACCCCACTTC 1512
Qy      1180 GTTACTAGA-----TTGAATCACCATGGAATGAGATCCCGTCTATACCTGTTT 1229
Db      1513 GATACTAGAGATTCATCTCTAGTTACCCCAATAGTATGATTCGATGTAAACTGTTG 1572
Qy      1230 GTACATATGATCAGATTGAGCGCGGTAGACTGAACATGCTATTTGTTGTTT 1287
Db      1573 TAAATAGGAGTAAGGTCAAGAAACATGGTAGATTGCGCACTTGTGTTGTTT 1630

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RESULT 6

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US-10-425-114-3164
; Sequence 3164, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 39-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3164
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Zea mays

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FEATURE:

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; OTHER INFORMATION: Clone ID: 700242603_FLI
US-10-425-114-3164

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Query Match      38.9%; Score 543; DB 7; Length 873;
Best Local Similarity 89.3%; Pred. No. 1.2e-147;
Matches 585; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy      537 CACTCGGCGAGCTGATCACCAGCGACCTGAAGCGCGAGCAACTGCTGCTGAACGCCAAC 596
Db      1 CACTCGGCGAACGTCATCACCAGCGACCTCAGCGCCAGCAACTGCTGCTGTAACGCCAAC 60
Qy      597 TCGGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCGCTGCTGCGAGAGCGACATGATG 656
Db      61 TCGGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCGCTGCTGCGAGAGCGACATGATG 120
Qy      657 ACGGAGTACGTGGTCAACCGCGGTGATCCGCGCGCGCGAGCTGCTGCTCAACTCCACCGAC 716
Db      121 ACGGAGTACGTGGTCAACCGCGGTGATCCGCGCGCGCGAGCTGCTGCTCAACTCCACCGAC 180
Qy      717 TACTCGCGCGCATCGAGCTGCTGGTCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
Db      181 TACTCGCGCGCATCGAGCTGCTGGTCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy      777 CAGCGCTCTTCCCGCGGAGGACCAACATGACAGATGCGCTCATACCGAGGTGATC 836
Db      241 CAGCGCTCTTCCCGCGGAGGACCAACATGACAGATGCGCTCATACCGAGGTGATC 300
Qy      837 GCGGACCGCGACCGAGCGAGCTGGGGTTTCATACGGAACGAGGACGCGAGGAGTACATG 896
Db      301 GCGGACCGCGACCGAGCGAGCTGGGGTTTCATACGGAACGAGGACGCGAGGAGTACATG 360
Qy      897 AGGCACTTCGCGAGTACCCCGCGGAGCTTCGCGGAGCATGTTCCCGGGTGCAGCC 956
Db      361 CGCACCTCCCGAGTTCGCGCGCGCGCTTCGTCAGCTTCGTCGCGGATGCGAGCC 420
Qy      957 GCGCGCTCGACTCATCGAGAGGATGCTCACCTTCAACCCGCTGAGAGATCAGATT 1016
Db      421 GTCGCGTGGATCTCATCGAGCGGATGCTCACCTTCAACCCGCTGAGAGGATCAGATT 480
Qy      1017 GAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGACAGCATCCCGATGAGCCCATC 1076
Db      481 GAAGAGCGCTGGAGCACCCGTCACCTGGAAACGCTACAGCGTCCCGCGAGCCCATC 540
Qy      1077 TCGCTGGAGCCCTTCCTTCGACTTCGAGCGAGAGGCTCTTAAACGAGACCAATGAAG 1136
Db      541 TGACGAGCCCGTTCGTTTCGACTTCGAGCAGCAGGCTCTGACGGAAGACCAATGAAG 600
Qy      1137 CAGCTGATCTTCAACGAGCGATCGAGATGAACCCCAACATCCGCTACTAGATTG 1191
Db      601 CAGCTGATCTTCAACGAGCGCATCGAACTCAACCCCAACTTCGGAATAGCTAGTAG 655

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RESULT 7

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US-09-938-842A-644
; Sequence 644, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22

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Qy	1101	TTGAGCAGAGGCTCTAAACGAGACCAAAATGATGAGCTGATCTTCAACGAAACGATC	1160
Db	1241	TTTGAGCAACCATCTTTACAGAGCGCATATAAAGAACTTATCTGGAGGGAATCTTTTA	1300
Qy	1161	GAGATGAACCCAAACATCCGGTACTAGATTGAA	1193
Db	1301	GCATTTAACCCGGATCTCTCCCTACTAATTCAA	1333

RESULT 10

US-10-767-701-14217

; Sequence 14217, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 14217

; LENGTH: 1707

; TYPE: DNA

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41_1

US-10-767-701-14217

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RESULT 11
US-10-425-114-28439
Sequence 28439, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28439
LENGTH: 1520
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4759-036-H6_FLI
US-10-425-114-28439

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	Query Match	34.8%	Score 485.8;	DB 7;	Length 1520;
	Best Local Similarity	64.8%;	Pred. No. 7.8e-131;		
	Matches 721;	Conservative	0;	Mismatches 392;	Indels 0; Gaps 0;
Qy	81	GACGGGGCGCGGTGGCGAGTTTCAGGCGCGACGATACGACGCGCGCGCGGTACCTGCTC	140		
Db	38	GGCGGGCGCGGTGGACGCGACGATCAAGGGTATGGCGACGACGCGGGCGCGCTACGTGCTG	97		

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QY 141 TACGACATCTTCGGGAAACAGTTTCGAGGTGACGAAACAGTACACGCGCCCATCATGCC 200
Db 98 TACAACGTGTACGGGAACCTCTTCGAGGTCTCTCCAAAGTACGCCCAACCCATCCGCCCC 157
QY 201 ATTGGCCGGGGCCCTACCGGATCGTCTCGTGATGAACCTTTGAGACGAGGAGATG 260
Db 158 ATCGGTCCGGCCCTACGGCATTTGTCTGGGGGTCTCACTCGCAGTCAGGGAGGAG 217
QY 261 GTGGCGATAAAGATAGTCCCAACCGGTTCAACACGACATGACGCCAAGCGCAGCTC 320
Db 218 GTTTCGATCAAGAAGTTTGGCAATGCGTTTCGAAACACATGACGCCAAGCGCAGCTC 277
QY 321 CGGAGATCAAGTCTCTCAGGCACTTCGACGACGAAACATCATAGGCATCAGGATG 380
Db 278 AGGGAATCAAGTCTCGGCCACATGGACCATGAGACATCTCTGCCCTTAAAGGATGA 337
QY 381 ATCCCGCCCGCATCCCTCAGGCGTTTCAACGAGCTCTACATCGCCACGCGAGTCTATGGAC 440
Db 338 ATTCCGCCCCCACTAGAGAGAACTTTAATGAGTGTACATTTGTTACTGAGTTAATGGAT 397
QY 441 ACCGACCTCATCATCATCTCCGCTCCAAACGAACTGTCTGAGAGACGACTGCCAGTAT 500
Db 398 ACAGATCTCCATCAGATCGTACGCTCAATTCAGCCATTGACTGATGATCATTTGCCAGTAC 457
QY 501 TTTCTGTACGATCTCGGGGGCTCAAGTACATCCACTCGCGAAGCTGTATCCACCGC 560
Db 458 TTTCTGTATCAGTTTACGAGGGCTTAAATATGTGCACTCAGCAATATATTTGCCACCG 517
QY 561 GACCTGAAGCCGAGCAACTCTGCTGTAACGCGCACTCGGACCTCAAGATCTCGCACTTC 620
Db 518 GATCTGAGCCGAGCAATTTGTTCTTAATGCAATTTGACTCAAGATTGCACTTT 577
QY 621 GGGCTCGCGCGCGCTCGTTCGAGAGCGCATGATGACGAGTACGTGTCTACCCGGTGG 680
Db 578 GGGCTTTCGAAAGCACTTCAGAGACAGATCTCATGACAGAGTATGTGTCTCACTGTTGG 637
QY 681 TACCGCGCGCGAGTCTGCTCAACTCCACGACTACTCCGCGCGCATCGAGTCTGG 740
Db 638 TACCGGGCACGAGCTGCTGTGTAATCTGTTCACTGACTACTGCTGCCATTGATGCTGG 697
QY 741 TCCGTGCGGTGATCTTTGAGAGTCACTCAACCGCGCAGCGCTCTTCCCGCGAGGAG 800
Db 698 TCAAGTTGGATGATATAGTGAATCGTTACTGTCGTAACCCCTGTTTCTGAGCGGAT 757
QY 801 CACATGACGAGATGCGCTCATCACGAGGTGATCGGACGCGCGAGCGAGCAGAGCTG 860
Db 758 TACATCCAGCAATTAATAATTGATCACTGAGCTCATAGGCTCTCCAGATGATGCAAGCTG 817
QY 861 GGGTTTCATAGGAAACGAGGACGAGGAGTACATGAGGCACTGCGCGAGTACCGCGC 920
Db 818 GGATTTCTTGAAGTGATTAATGCAAAAGATACATGAAACAACTACACAGTTTCCAAAG 877
QY 921 CGGAGCTTTCGAGCATGTTCCCGGGTGCAGCGCGCGCTCGACCTCATCGAGAGG 980
Db 878 CAGGACTTCGCGCTGTTCCGACATGCTCTCTGGCGAGTCAATTTGTTGGAAAGG 937
QY 981 ATGCTCACCTTCAACCGCTGACAGAAATCAGAGTTGAGAGGCGCTCGCATCATCTTAC 1040
Db 938 ATGCTTGTGTTGATCCAAAGCAGACGGAATTAAGTTGATGAGGCTCTGCAATCATCATAC 997
QY 1041 CTAGAGAGATTGACGACATCGCGGATGAGCCCATCTGCTGAGGCGCTTCTCTCTGAC 1100
Db 998 TTGGCTTTCATCTCATGAGATCAATGATGAACCTTACCTGCGCTGCACCTTTTCACTTGTAT 1057
QY 1101 TTGAGCAGAGGCTCTTAAACGAGGACCAATCAAGCAGCTGATCTTCAACGAAGCGATC 1160
Db 1058 TTTGAGCAACCATCTTTTACAGAGCGCATATAAAGAACTCATCTGGAGGGAATCTTTA 1117
QY 1161 GAGATGAACCAACATCTCGGTACTAGATTGAA 1193
Db 1118 GCATTTAAACCCAGAGCTCCCTACTAATCAAA 1150
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RESULT 12
US-10-425-115-86951/c
; Sequence 86951, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 86951
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179305C.1
US-10-425-115-86951

Query Match 34.8%; Score 485.8; DB 8; Length 1803;
Best Local Similarity 64.8%; Pred. No. 8.4e-131;
Matches 721; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

QY 81 GACGGGCGCGCGTGGCGAGTTTCAGCGCGAGTACGACGCGCGCGCGTACCTGCTC 140
Db 1524 GCGCGCGCGGTGGAGCGCAGATCAAGGTATGGCGAGCAGCGGGCGCTAGCTGCTG 1465
QY 141 TACGACATCTTCGGGAACAGTTTCAGGTGAGCAAGTACGACGCGCGCGCATGCCCC 200
Db 1464 TACAACGTGTACGGAACCTCTTCGAGGTCTCTCCAGTACGCGCCCACTCCGCCCC 1405
QY 201 ATTGGCGCGCGCGCTAGCGGATCGTCTCGTGATGAACTTTGAGACGAGGAGATG 260
Db 1404 ATCGGTGCGCGCGCTTACGCGATTTGTCTCGCGGTGTCTCACTCGCAGTCAGGGAGGAG 1345
QY 261 GTGGCGATAAAGAAGATCGCCAAACCGTTTCAACAGCATGAGACGCCAAGCGCAGCTC 320
Db 1344 GTTCGATCAAGAAGTTGGCAATGCTTCGACCAACACATCGACGCCAAGCGCAGCTC 1285
QY 321 CGGAGATCAAGCTCTCAGGCACTCGACCAAGCAATCATAGGCAATCAGGAGTGTG 380
Db 1284 AGGGAATCAAGTCTGTCGCCACATGGACCATGAGCAATCTTGGCTTTAAAGGATGA 1225
QY 381 ATCCCGCGCGCATCCCTCAGGCGTTTCAACGAGCTCTACATCGCCACGAGCTCATGGAC 440
Db 1224 ATTCCGCCCCCACTAGAGAGAACTTTAATGAGTGTACTTTGTTACTGAGTTAATGGAT 1165
QY 441 ACCGACCTCCATCATCATCTCCGCTCCAAACCAAGAACTGTCTGAGAGACGACTGCCAGTAT 500
Db 1164 ACAGATCTCCATCAGATCGTACGCTCAATCAGCCATTGACTGATGATCATTCAGGAGTAC 1105
QY 501 TTCCTGTACAGATCTCGGGGGCTCAAGTACATCCACTCGCGGAAACGTGATCCACCGC 560
Db 1104 TTTCTGTATCAGTTGCTACGAGGGCTTAAATATGTGCACTCAGCAATATATTTGCAACCGC 1045
QY 561 GACCTGAAGCCGAGCAACTGCTGTAACGCGCACTGCGACTCAAGATCTCGGACTTC 620
Db 1044 GATCGAAGCCGAGCAATTTGTTCTTAAATGCAATTTGAGCTCAAGATTGAGACTTT 985
QY 621 GGGCTGCGCGCGCGCTGTCGGAGAGCGCATGATGACGAGGATCGTGGTTCACCCGGTGG 680
Db 984 GGGCTTGAAGGAGCCACTTTCAGAGACAGATCTCATGACAGAGATATGTGTCTACTCGTGG 925
QY 681 TACCGCGCGCGAGGCTGCTCAACTCAACCGACTACTCCGCGCGCATTCGACGCTG 740
Db 924 TACCGGCGACAGAGCTGCTGTTGAACCTTTCACAGTATCTGCTGCCATTTGATGTCTGG 865
QY 741 TCCGTGCGGTGCTCTTTCATGGAGCTCATCAACCGCGCGCGCTCTTCCCGCGCAGGAC 800
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Db 864 TCAGTTGGATGACATACAGTGAATCGTTACTCGTCAACCCCTGTTTCTCGACGGGAT 805
Qy 801 CACATCACAGATCGCTCATCACGAGGTGATCGGAGCGCGACGACGAGCTG 860
Db 804 TACATCAGCAATTAATTAATGATCCTGAGCTCATAGGCTCTCCAGATGATGCAAGCCTG 745
Qy 861 GGGTTCATACGGAACGAGGACGCGAGGAAGTACATAGGACCTGCGCAGTACCGCGC 920
Db 744 GGATTTCTTGAAGTGATAATGCAAAAGATACATGAACAACATACCAAGTTTCCAAGA 685
Qy 921 CGGACGTTCCGAGCATGTTCCGCGGTTGAGCCCGCGCTCGACCTCATCGAGGG 980
Db 684 CAGGACTTCCGCTCGCTTTCGCAACATGTCTCTGGCGCAGTCGATTTGTTGGAAGG 625
Qy 981 ATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTTGAGGAGCGCTCGATCATCTTAC 1040
Db 624 ATGCTTGTTGATCCAGCAGACGGATTACAGTTGATGAGGCTCTGCATCATCCATAC 565
Qy 1041 CTAGAGAGATTGACGACATCGCGATGAGCCCATCTGCTCGAGCCCTTCTCTTCGAC 1100
Db 564 TTGGCTTCACTTCATGAGATCAATGATGAACCTTACCTGCCCTGCACCTTTTCAGCTTTGAT 505
Qy 1101 TTGAGCAGAGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAGCGATC 1160
Db 504 TTGAGCAACCATCTCTTACAGAGCGCATATAAAAGAACTCATCTGAGGGAATCTTTA 445
Qy 1161 GAGTGAACCCAAACATCCGTTACTAGATTGAA 1193
Db 444 GCATTTAACCCAGAGCTCCCTACTAATATCAA 412

RESULT 13
US-10-437-963-36761/c
; Sequence 36761, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 36761
; LENGTH: 1717
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40555C.1
US-10-437-963-36761

Query Match 34.3%; Score 478.4; DB 7; Length 1717;
Best Local Similarity 64.4%; Pred. No. 1.2e-128;
Matches 716; Conservative 0; Mismatches 396; Indels 0; Gaps 0;

Qy 75 GGGATGAGCGGGCGCGGTGGCGGAGTTTCAGSCCAGCATGACGACGCGCGCGGGTAC 134
Db 1444 GGGCGGGCGCGCGCGCGCGCGCGAGATCAAGGGATGGGACGCGCGGGCGCGCTAC 1385
Qy 135 CTGCTCTACGACATCTTCGGGAACAAGTTGAGGTTGACGAACAAGTACGAGCGCGCCATC 194
Db 1384 GTGCTGTACAACTGTGACGGAACTTCTTCGAGGTCTCTCTCAAGTACGCGCCCTCCCATC 1325
Qy 195 ATGCCCATTTGGCGCGCGCTACGGGATCGTCTGCTCGTATGAACTTTGAGGAGG 254
Db 1324 CGCCCCATCGCGCGCGCGCTACCGCATTTGTCTGCGCGGCTGTTAACTCGGAGACGCG 1265

Qy 255 GAGATGTTGGGATAAAGAGATCGCCAAACGCTTCAAACAACGATCGAAGCCGAGCGC 314
Db 1264 GAGGAAGTTGGCAATCAAGAAGATTGGCAATGCAATTCGACCAACCATATCGATGCCAAGCGG 1205
Qy 315 AGCTTCCGGGAGATCAAGCTCTCAGGCACTTCGACCAACGAGAAACATCATAGGCAATCAGG 374
Db 1204 ACATCGAGAGAAATCAAGCTGCTTCGCCACATGAGCAACGAGAAATATTTATGCCCATAAG 1145
Qy 375 GATGTGATCCCGCGCGGATCCCTCAGCGGTTCAACGAGGTTCTACATCGCCACGAGCTC 434
Db 1144 GACATAATTCGCCCCCAAGAGAGACAACTTTAATGATGTTTACATTTCTGAGTTG 1085
Qy 435 ATGAGACCGGACCTTCATCATCATCCGCTCCAAACCAAGAACTCTCAGAAGAGCACTGC 494
Db 1084 ATGATATCTGATCTCCATCAGATCATACGCTCAATCAACCATTCGACTGATGACCACTGC 1025
Qy 495 CAGTATTTCTGTGTACAGATCTCGGGGGCTCAAGTACATCCATCTCGGCGAACTGATC 554
Db 1024 CAGTACTTCTGTACAGTTGCTACGAGGGCTAAATATATGTGCACTCGGCAAAATGCTTTG 965
Qy 555 CACCGGACCTGAGCGCGGCAACCTGCTGCTGTAACGCAACTGCGGCTCAAGATCTGC 614
Db 964 CACCGTATCTGAAGCCAAAGCAATTTGTTCTTAAATGCAAAATTTGATCTCAAGATTGCT 905
Qy 615 GACTTCGGGCTGGCGCGCGCTCGTTCGAGAGCGACATGATGACGAGTACGTTGCTCACC 674
Db 904 GATTTGGGCTTGCAGAAACCACTACGAGACTGACCTCATGACAGAGATATGTGCTACT 845
Qy 675 CGGTGATACCGCGCGCGGAGCTGCTCAACTCAACCGACTACTCGCGCGCACTGCAGC 734
Db 844 GCTTGGTATCGAGACACGAGCTGCTGTTGAATGCTCGCAGTATCTGCTGCTATTGAT 785
Qy 735 GTCTGCTCGCTCGCTGCTCTCATGAGCTCATCAACCGCGCGCTCTTCCCGCGC 794
Db 784 GTCTGCTCAGTTGGATGCTACTTGGTGAATTTGACTCGTCAACCCCTGTTTCTTGA 725
Qy 795 AGGACACATGACACGATCGCTCATCACCGAGGTGATCGGAGCGCGGACGCGGACGAC 854
Db 724 AGGATTTACATTCAGCAACTAAATTTGATCACTGAGCTGATAGGCTCGCCAGATCACTCA 665
Qy 855 GAGCTGGGGTTCTATACGGAACGAGGACGCGAGGAAGTACATGAGGCACTTCGCGGAGTAC 914
Db 664 AGCTAGGAGTTCTTCGAGGTGATAATGCAAGAAGATACATGAACAGCTACACAGTAC 605
Qy 915 CGCGCGCGGAGCTTCGCGAGCATGTTCCGCGGGTGCAGCGCGCGCTCGACCTCATC 974
Db 604 CCAAGGCGAGGACTTCCGCTTTCGCGCAACATGCTGCTGCTGCTGCTGCTGCTGTTA 545
Qy 975 GAGAGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTTGAGGAGCGCTCGATCAT 1034
Db 544 GAGAAATGCTGGTGTGACCCAGCAGACGGATACTGTTGATGAGGCTCTTCTATCAC 485
Qy 1035 CTTTACCTAGAGAGATTGACGACATCGCCGATGAGCCCATCTGCTGAGGCGCTTCTCC 1094
Db 484 CCATACTTGGGCTTCTTTCATGACATCAATGAAGAACCACCTCGCCAGCACCTTTTCAGC 425
Qy 1095 TTCGACTTCGAGCAGAGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAA 1154
Db 424 TTTGATTTGAGCAACCACTCTTTACTGAAGAACAATATAAAGAACTCATCTGGAGGAA 365
Qy 1155 GCGATCGAGATGAACCCAAACATCCGGTACTA 1186
Db 364 TCCTTGGCATTTAATCCGGATCCTCCCTACTA 333

RESULT 14
US-10-425-114-6328
; Sequence 6328, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jirong
; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack B
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 6328
 ; LENGTH: 1888
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700561155_FLI
 US-10-425-114-6328

Query Match 33.5%; Score 467.8; DB 7; Length 1888;
 Best Local Similarity 68.5%; Pred. No. 1.6e-125;
 Matches 646; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

QY	229	GCTCGTGATGAAC	TTTGAGACGAGGAGATGGCGGATAGAGATCCCAAGCGCT	288
DB	654	GCTCGCTGTGAAT	ACCGAGACGAATGAGCTGGTGGCGGTAAAGAAGATAGCAACGCTT	713
QY	289	TCAACAAAGCA	TGACGCCCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCG	348
DB	714	TCGACATCACA	TGACCGCTAAGCGTACGCTTCGTGAGATTAGTCTCTTAGGCATTGG	773
QY	349	ACCACGAAACAT	CATATAGCGATTCAGGATGTGATCCCGCCGCGATCCCTCAGCGGTCA	408
DB	774	ATCATGAAATG	TAAATGCTTTGAGAGATGTAATTCCTCCACCCTTCGCTGAGAGATTGA	833
QY	409	ACGAGCTCTAC	ATCCGACGGAGCTCATGGACCGGACCTCCATCATCATCCGCTCCA	468
DB	834	ATGATGTCTAC	ATAGCCACTGAATCATGGATCTGATCTTCCACCATCATCTTCGCTCCA	893
QY	469	ACCAAGAACTG	TCAAGAGCACTGCCAGTATTTCTGTACCAAGATCCTCGCGGGCTCA	528
DB	894	ATCAAAATCTG	TACAGGAGCACTCTCAATACTTTCTGTACCAAGTCTTCGTGGGCTTA	953
QY	529	AGTACATCCA	CTCGGCGAACGTGATFCCAACCGCACCTGAAAGCGAGCAACCTCTCTCTGA	588
DB	954	AGTATATAC	TATCTCGAAACGTAATCCATAGAGATTTAAACCAACCACTCTCTGTAA	1013
QY	589	ACGCCAACTGC	ACACTCAAGATCTCGGACTTCGGGCTGGCGCGCGCTCTCTCGGAGCG	648
DB	1014	ACTCAAATTTG	CACTTGAAGATTATGATTTTGGTCTTCGGAGACCAACTTTGGAAGTG	1073
QY	649	ACATGATGAC	GAGTACGTGGTTCACCCCGTGTATCCGCGCGCGGAGCTCTCTCAACT	708
DB	1074	ACTTCATGAC	AGAAATATGTAGTCAACAATGGTACAGATCTCCGAATGTGTGTGAAT	1133
QY	709	CCACCGACTAC	TCTCCGCGCCATTCGACGCTCTGGTCCGTGGCTGTCATCTTCATGGAGTCA	768
DB	1134	CCTCTGATTAC	ACCTCTGCTATAGATGTGTCTGTGTGGTTGTCATCTTTATGAGCTTA	1193
QY	769	TCACCGCGAC	CGCGCTCTTCCCGGACGGGACACATGCACAGATGGCGCTCATACCG	828
DB	1194	TGAATAAAAG	CGCTCTGTCTTCGGGCAAGACCATGTGTCATCAGATCGCTTATTGACAG	1253
QY	829	AGGTGATCGG	ACGCGGACGACGAGCTGGGGTTCATACGAAACGAGGACCGGAGGA	888
DB	1254	AGCTCTTGGC	ACCCCAACTGAGGCTGACCTTGGGTAGTGAAAAATGAAGATGCAAGAA	1313
QY	889	AGTACATGAG	CACTGCGCAGTACCCGCGCGGACGTTCCGAGCATGTCTCCCGCGG	948
DB	1314	GATATATCAG	AACTTCTCAATATCTTCGCAACCTTTAGCTCAAGTCTTCCCCCATG	1373
QY	949	TGCAGCCCGC	CGCGCTCGACCTCATCGAGAGGATGCTCACTTCAACCCCGCTGAGAGAA	1008
DB	1374	TTTCATCCGC	AGCCATTTGATCTTTGTGATAAAATGTTGACAGTTGATCCCAACCAAGAA	1433

Qy 1009 TCAAGTTGAGGAGCGCTCGATCATCTTACCTAGAGAGATTCACGACATCGCCGATG 1068
 Db 1434 TTAAGTTGAAGAAGCACATAGCCCATCCATCTTGAAAAACTGCATGATGTAGCTGATG 1493
 Qy 1069 AGCCCATCTCGCTGGAGCGCTTCTTCCTTCGACTTCGAGCAGAAGGCTCTTAAACGAGGACC 1128
 Db 1494 AACCAATCTGCATGGAGCCATTTTCATTTGATTTTGGAGCAACAACAATTTGGATGAAGAGC 1553
 Qy 1129 AAATGAAGCAGCTGATCTTTCACGAGAGCGATCGAGATGAACCC 1171
 Db 1554 AAATAAAGAGATGATCTTACAGGAAGCATTTAGCACTCAATCC 1596

RESULT 15
 US-10-424-599-141942
 ; Sequence 141942, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 141942
 ; LENGTH: 1969
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_99188C.1
 US-10-424-599-141942

Query Match	33.5%;	Score 467.8;	DB 7;	Length 1969;
Best Local Similarity	68.5%;	Pred. No. 1.6e-125;		
Matches 646;	Conservative 0;	Mismatches 297;	Indels 0;	Gaps 0;
Qy	229	GCTCCGTGATGAACTTTGACACGAGGGAGATGTGGCGATAAAGAGATCGCCAAACCGGT	288	
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Qy	289	TCAACACGACATGAGCCGACCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCG	348	
Db	723	TCGACATCAGATGGACGCTAAGCGTAGCTTCTGTGAGATTAGCTTCTTAGGCATTTGG	782	
Qy	349	ACCAACGAGAAATCATATAGGCATCAGGGATGTGATCCCGCCGATCCCTCAGCGCTTCA	408	
Db	783	ATCATGAAATGTAAATTGGTTTGAGAGATGTAATTCCTCCACCTTGCGTAGAGAGTTTA	842	
Qy	409	ACGACGCTTACATGCCACCGAGCTCATGACACCGACCTCCATCATCATATCCGCTCCA	468	
Db	843	ATGATGTCATAGACCACTGAATCTCATGGATACTGATCTTTCACCATATCAATCGCTCCA	902	
Qy	469	ACCAAGAACTGTCAGAGAGCACTGCCAGATATTTCTGTACCAAGATCCTCGGGGGCTCA	528	
Db	903	ATCAAAATCTGTTCAGAGAGGACCTCTCAATACTTTCTTGTACCAAGATCTTCGTGGGGCTTA	962	
Qy	529	AGTACATCCACTCGGCGAAACGTGATCCACCGCGACCTGAAGCCGAGCAACCTGCTGCTGA	588	
Db	963	AGTATATACATTTCTGCAAAACGTAAATCATAGAGATTTAAACCAAGCAACCTGCTGCTAA	1022	
Qy	589	ACGCCAACTGCGACCTCAAGATCTGCGACTTCGGGCTGGCGCGGCCCGTCTCGGAGAGCG	648	
Db	1023	ACTCAAATTTGACTTCAAGATTATTGATTTTGGTCTCTTCGCGAGACCAACTTTTGGAAAGTG	1082	
Qy	649	ACATGATGACGGAGTACGTGGTACCCCGGTGGTATACCGCGCGCCGGAGCTGCTGCTCAACT	708	
Db	1083	ACTTCATGACAGAAATGTGTAGTCAACAAGATGGTACAGAGCTCCCGAAATTTGTTTGAATT	1142	

Qy	709	CCACCGACTACTCGCGCCGACATCGACGTCGTGCTCGGCTGCTCATCTTTCATGAGCTCA	768
Db	1143	CTCTCGATTACACCTCTGCTATAGATGTGTGCTGTGTTGTCATCTTTATGGAGCTTA	1202
Qy	769	TCACCGCCAGCGGCTCTTCCCGGCGAGGACACATGACACAGATGCGCCTCATCACCG	828
Db	1203	TGAATAAAAGCCTCTGTTCGCGGCAAGACCATGTGCATCAGATGCGCTTATTGACAG	1262
Qy	829	AGGTGATCGGGAGCGCGACGACGAGCTGGGGTTTCATACGGAACGAGGACGCGAGGA	888
Db	1263	AGCTTCTTGGCACCCCAACTGAGGCTGACCTTGGGTTAGTGAAAATGAAGATGCAAGAA	1322
Qy	889	AGTACATGAGGCACCTGCGCGACGTACCGCGCGGACGTTTCGCGAGCATGTTCCCGCGGG	948
Db	1323	GATATATCAGACAACCTTCTCAATATCTCTCGCCAACTTTAGCTCAAGTCTTCCCCCATG	1382
Qy	949	TGCAGCCCGCGGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCGCTGCGAGAA	1008
Db	1383	TTCATCCGGCAGCCATTGATCTTGTGATAAAATGTTGACAGTTGATCCCAAAAGAA	1442
Qy	1009	TCACAGTTGAGGAGCGCTCGATCATCTTACCTAGAGAGATTGCAAGACATCGCGATG	1068
Db	1443	TTACAGTTGAAGAGCACATAGCCCATCCATACCTTGAAAACTGCATGATGTAGCTGATG	1502
Qy	1069	AGCCCATCTGCTGGAGCCCTTCTCTTCGACTTCGAGCAGAGGCTCTAAACGAGGACC	1128
Db	1503	AACCAATCTGCATGGAGCCATTTTCATTTGATTTTGAGCAACAACAAATTGGATGAAGGC	1562
Qy	1129	AAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCC	1171
Db	1563	AAATAAAGAGATGATCTACAGGGAAGCATTAGCACTCAATCC	1605

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Job time : 843 secs

GenCore version 5.1.6
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(without alignments)
3752.939 Million cell updates/sec

Title: US-10-768-886-1
Perfect score: 1396
Sequence: 1 gagagtcagataagtcgt.....ttaaaaaaaaaaaaaaa 1396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4172979 seqs, 262114271 residues
Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*
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8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337.2	24.2	1866	6	US-10-955-054A-5
2	278.8	20.0	1888	6	US-10-770-726-25
3	258	18.5	1611	7	US-11-186-284-114
4	234	16.8	2737	6	US-10-909-125-861
5	161.4	11.6	2525	6	US-10-770-726-5
6	141	10.1	2372	6	US-10-857-780-11
7	135.4	9.7	3131	6	US-10-770-726-28
8	128	9.2	983	6	US-10-770-726-9
9	104.2	7.5	2328	6	US-10-770-726-7
10	95.6	6.8	3073	7	US-11-113-424-11
11	92	6.6	1400	6	US-10-750-185-28925
12	75.8	5.4	1474	6	US-10-770-726-8
13	63.6	4.6	2838	6	US-10-770-726-27
14	63	4.5	2497	6	US-10-750-185-35100
15	60.4	4.3	3527	6	US-10-770-726-35
16	59.8	4.3	1254	6	US-10-966-483-32
17	59.8	4.3	1254	7	US-11-021-441-16
18	59.8	4.3	1392	7	US-11-000-365-49
19	59.8	4.3	1392	7	US-11-032-794-49
20	59.8	4.3	1437	6	US-10-966-483-35
21	59.8	4.3	1437	7	US-11-021-441-19
22	59.8	4.3	3105	6	US-10-966-483-19
23	59.8	4.3	3105	7	US-11-021-441-3

24	59.8	4.3	3963	6	US-10-966-483-1	Sequence 1, Appli
25	59.2	4.2	1636	6	US-10-981-029-6	Sequence 6, Appli
26	57.6	4.1	1639	6	US-10-770-726-21	Sequence 21, Appl
27	57.4	4.1	5221	6	US-10-821-234-367	Sequence 367, App
28	57.2	4.1	2030	7	US-11-111-239-1	Sequence 1, Appli
29	57	4.1	1371	6	US-10-451-375-5	Sequence 5, Appli
30	57	4.1	3832	6	US-10-821-234-99	Sequence 99, Appl
31	55.4	4.0	5745	6	US-10-750-185-54380	Sequence 54380, A
32	54.8	3.9	2545	7	US-11-099-691-15	Sequence 15, Appl
33	54.2	3.9	1065	6	US-10-451-375-1	Sequence 1, Appli
34	52.6	3.8	1142	6	US-10-750-185-58025	Sequence 58025, A
35	52.6	3.8	2310	7	US-11-073-579-1	Sequence 1, Appli
36	52	3.7	1593	6	US-10-858-730-138	Sequence 138, App
37	52	3.7	1680	6	US-10-770-726-37	Sequence 37, Appl
38	51.8	3.7	6058	6	US-10-770-726-17	Sequence 17, Appl
39	51.4	3.7	1278	6	US-10-750-185-52966	Sequence 52966, A
40	51.2	3.7	1427	6	US-10-770-726-11	Sequence 11, Appl
41	50.8	3.6	6890	7	US-11-005-029-1	Sequence 1, Appli
42	50.6	3.6	409	7	US-11-108-172-176	Sequence 176, App
43	49.6	3.6	3513	6	US-10-858-730-142	Sequence 142, App
44	49.2	3.5	2213	6	US-10-770-726-31	Sequence 31, Appl
45	49.2	3.5	35893	6	US-10-860-436-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-955-054A-5
; Sequence 5, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AVERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:8800S
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-5

Query Match	24.2%	Score	337.2	DB	6	Length	1866
Best Local Similarity	61.3%	Pred. No.	8.3e-68				
Matches	603	Conservative	0	Mismatches	363	Indels	18
Gaps	3						
Qy	182	CCAGCGCCCATCATGCCATTCGGCGCGCGCTACGGGATCGTCTGCTCGGTGATGAA	241				
Db	195	CTACAGCGAGTTCGAGTACATCGCGAGGCGCGGTACGGATGCTCAGCTCGGCCTATGA	254				
Qy	242	CTTTGAGACGAGGAGATGTTGGCGATAAAGAGATCGCCACCGCTTCAACACGACAT	301				
Db	255	CCAGGTGCGCAAGACTCGCGTGCATCAAGAGAT--CAGCCCTTCGAACATCAGAC	311				
Qy	302	GGAGCGCAAGCGCACGCTCGGGAGATCAAGCTCCTCAGGCACCTCGACACAGAACAT	361				
Db	312	CTACTCCAGCGCACGCTCGGGAGATCCAGATCTCTGCTGCGCTTCGCGCATGAGATGT	371				
Qy	362	CATAGGCATCAGGAGTGTATCCCGCGCGGATCCCTCAGGCGGTCAACGACGTCTACAT	421				
Db	372	CATCGGCATCCGAGACATTCCTCGGGCGTCCACCTGGAGCCATGAGATGTCTACAT	431				
Qy	422	CGCAGCGAGCTCATGGACACCGACCTCCATCATCATCATCCGCTCCCAACCAAGAGTGC	481				
Db	432	TGTCAGGACCTGATGGAGACTGACCT---GTACAGTTGCTGTAAGCCAGCAGCTGAG	488				

QY	482	AGAAGAGCACTGCCAGTATTTCTGTACCAAGATCTCTGGGGGCTCAAGTACATCCACTC	541
Db	489	CAATGACCATATCTGCTACTTCTCTTACCAAGATCTCTGGGGGCTCAAGTACATCCACTC	548
QY	542	GGGAAAGTATCCACGGGACCTGAAGCGGAGCAACTGTGCTGCTGAAGCCCACTGCGA	601
Db	549	CGCAACGCTCTCCACCGAGATCAAAGCCCTCAACCTGCTCAGCAACACCACTGCGA	608
QY	602	CCTCAAGATCTGGGACTTGGGCTGGCGGG-----CGTCTGCGAGAGCGA	649
Db	609	CCTTAAGATTTGATTTTGGCTTGGCCCGCGATGCGCGATCTTGAAGCATGACACACCGG	668
QY	650	CATGATGACGGAGTACGTGTCAACCGGTGTGACCGCGCGCGAGCTGTGCTCAACTC	709
Db	669	CTTCTGACGGAGTATGTGCTAGCGCTGGTACCGGGCCCGAGATCATGCTGAATC	728
QY	710	CACCGACTACTCGCGCGCATGACGTCTGGTCCGTGGCTGCTGATCTTCAATGAGTCTAT	769
Db	729	CAAGGCTATACCAAGTCCATGACATCTGGTCTGGGCTGCTATTTCTGGCTGATGCT	788
QY	770	CAACGCCAGCGCTCTTCCCGGAGGAGCACATGACACAGATGCGCTCATCACGA	829
Db	789	CTCTAACCGGCCCATCTTCTTGGCAAGCACTACCTGGATCAGCTCAACATCTTGGG	848
QY	830	GCTGATCGGAGACCGGACGAGACGAGCTGGGGTTTATACGGAACGAGGACCGAGGAA	889
Db	849	CATCTGGGCTCCCATCCAGGAGGACCTGAATTTGATATCAACATGAAGCCCGGAA	908
QY	890	GTACATGAGCACTCGCGAGTACCGCGCGCGGAGCTTGGGAGATGTTCCGCGGT	949
Db	909	CTACCTACAGTCTCTGCCCTCCAGACCAAGTGGCTTGGGCCAAGCTTTTCCCCAAGTC	968
QY	950	GCAGCCCGCGCTCGACTCATCGAGAGGATGCTCACTTCAACCCGCTGCAGAGAT	1009
Db	969	AGACTCAAAGCCCTTGACTGCTGGAACCGGATGTTAACTTTAACCCCAATAACGGAT	1028
QY	1010	CACAGTTGAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGCAGACATCGCCGATGA	1069
Db	1029	CACAGTGGAGGAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGAGATGA	1088
QY	1070	GCCCATCTGCTGGAGCCCTTCTCTTGAATTCGAGTGGAGAGAGGCTTAAACGAGACCA	1129
Db	1089	GCCAGTGGCGAGGAGCCCTTCACTTTCGCCATGGAGCTGGATGACCTACCTAAGGAGCG	1148
QY	1130	AATGAAGCAGCTGATCTTCAACGA	1153
Db	1149	GCTGAAGGAGCTCATTTTCAGGA	1172

RESULT 2
US-10-770-726-25
; Sequence 25, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-25

Query Match 20.0%; Score 278.8; DB 6; Length 1888;
Best Local Similarity 56.5%; Pred. No. 1.7e-54;
Matches 586; Conservative 0; Mismatches 437; Indels 15; Gaps 3;

QY	149	CTTGGGAAACAAGTTTCGAGGTGACGAACAAGTACAGCGGCCCATCATGTCCTTGGCGG	208
Db	137	CGTCAACAGACCGCTGGAGCTGCCCAAGACCTACGTGTCCCAGACGACGTCGGCAG	196
QY	209	CGGCGCTTACCGGATTCGTCTGCTCGTGAATGAACCTTTAGACGAGGAGATGGTGGCAT	268
Db	197	CGGCGCTTATGGCTCGGTGTCTGGCCATCGACAAGCGGTCAAGGGAGAGGTGGCCAT	256
QY	269	AAAGAGATCGCCAAACGGTTCAACAGCATGGAAGCCGAGCGACGCTCCGGAGAT	328
Db	257	CAAGAAGCTGAGCGACCTTTTCACTCGAGATCTTCCCAAGCGCGCTTACCGGAGCT	316
QY	329	CAAGCTCTCTCAGGCACTTCGACCAAGAGAAATCATAGGCATACAGGATGTGATCCCGC	388
Db	317	GCTGCTGTGAAGACATGAGCATGAGAAAGTCAATTGGGCTCTGGATGTCTTCACCCC	376
QY	389	GCCGATCCCTCAG---GGTTCAACGAGCTTACATCGCCACGAGCTCATGGAACCGA	445
Db	377	AGCTCTCTCCCTGCGCAACTTCTATGACTTCTACCTGGTGTGCTTCTATCGACAGGA	436
QY	446	CCTCATCATCATCTCCGCTCCNACCAAGAACTGTCAAGAGCACTGCCAGTATTTCT	505
Db	437	TCGAGAGATTCATGGG-----GATGGAGTTCACTGAGGAGAAAGTCCAGTACCTGT	490
QY	506	GTACCAAGATCTCGGGGGCTCAAGTACATCCACTCGCGCAACGTGATCCACCGGACCT	565
Db	491	GTATCAGATGCTCAAGGCTTTAGTACATCCACTCTCTGCTGGGTCTGTGCACAGGACCT	550
QY	566	GAAGCCGAGCAACTGTGTGTGAACGCACTCGGACCTCAAGATCTCGGACTTCGGGT	625
Db	551	GAAGCCAGCAACTGTGTGTGAATGAGGACTGTGAACCTGAAGATTTCTGGATTTTGGGT	610
QY	626	GGCGGGCGCTCGTCGAGAGAGGACATGATGACGAGTACGTGTGTCACCGGTGTACCG	685
Db	611	GGCGGAC-----ATGCAGACCGCGAGATGATGTGGTACGTGTGTGACCGCTGTACCG	664
QY	686	CGCGCGGAGCTGTGCTCAACTCCACGACTTACTCCCGCCGACATCGACGCTGTGTCCGT	745
Db	665	AGCCCCGAGGTGATCTCTCAGCTGGTGCATTAACACGACAGTGGACATCTGTGTCTGT	724
QY	746	CGGTGTCACTTTCATGGAGCTCATCAACCGCAGCGCTCTTCCCGCAGGAGCACCAT	805
Db	725	GGGTGTATCATGGCAGAGATGTGCACAGGGAATACTCTGTTCAGAGGGGAAAGATTACCT	784
QY	806	GCACAGATCGCTCATCAACGAGTGTGAGGAGCGGACGAGCAGCAGCTGGGTT	865
Db	785	GGACCACTGACCCAGATCTCTGAAGTACCGGGGTGCTTGGCACGGAGTTTGTGCAGAA	844
QY	866	CATACGGAAACGAGGACGAGGAGTACATGAGGCACTCGCGCAGTACCCCGCGGAC	925
Db	845	GCTGAACAGCAAGCGGCCAAATCTATCCAGTCTCTGCACAGACCCCGCAGNAGA	904
QY	926	TTTCGAGAGCATTTTCCCGGGTGCACCGCGCGCTCGACCTTCATCGAGAGATGCT	985
Db	905	TTTCACTCAGCTGTTCACCGCGCAGCCCCCAGGCTCGGACCTGTCTGGAGAGATGCT	964
QY	986	CACCTTCAACCGCTGCGAGAGATACAGTTGAGAGGGGCTCGATCATCTTACCTAGA	1045
Db	965	GGAGCTAGACCTGGCAAGCGCTGACCGCGCGCAGGCGCTTCACTTCTTTGA	1024
QY	1046	GAGATTGACACATCGCGGATGAGCCCATCTGCTGGAGCGCTTCTCTCTCGATTCGA	1105
Db	1025	ACCTTTCGGGACCTTGAGGAAGAGACGAGGCGCCAGCAGCGCTTGTGATTCCTTAGA	1084
QY	1106	GCAGAGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTTCACAGAGGATCGAGAT	1165
Db	1085	ACACGAGAACTCAAGTGGATGAATGAAGCAGCACATCTACAGGAGATTGTGAATCT	1144
QY	1166	GAACCCCAACATCCGTA	1183
Db	1145	CAGCCCCATTCGCCGAA	1162


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RESULT 3
US-11-186-284-114
; Sequence 114, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgard, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (328)....(1410)
US-11-186-284-114

Query Match      18.5%; Score 258; DB 7; Length 1611;
Best Local Similarity 55.7%; Pred. No. 9.1e-50;
Matches 564; Conservative 0; Mismatches 430; Indels 18; Gaps 3;

QY 191 CATCATGCCCATTTGGCGCGCGCGCTACGGGATGCTGCTCGGTGATGAACCTTTGAGAC 250
DB 408 CCTCTCGTACATCGCGGAGGCGCTACGGCATGGTGTCTGCTTATGATAATGTCAA 467
QY 251 GAGGAGATGTTGGCGGTAAGAAGATCGCCAGCGCTTCAACACACATGCGCCAA 310
DB 468 CAAAGTTCGAGTAGTATATCAAGAAAT---CAGCCCCCTTTGAGCACCAGACCTACTGCCA 524
QY 311 GCGCAGCTCCGGGAGATCAAGTCTCTCAGGCACTCGACACAGAGAAATCATATAGGCAT 370
DB 525 GAGAACCTGAGGAGATAAATCTTACTCGGCTTCAGACATGAGAACATCATTTGGAAT 584
QY 371 CAGGAGATGATCCCGCGCGCGATCCCTCAGGCGTTCAACGAGCTTACATCGCCAGCA 430
DB 585 CAATGACATTTTCGAGCACCACCATCGAGCAATGAAAGATGATATATAGTACAGGA 644
QY 431 GCTCATGAGCACCAGACCTCCATCATCATATCCGCTCCAAACAGAACTGTACAGAGCA 490
DB 645 CCTCATGGAACAGATCT---TTACAAAGCTCTTTGAAGACACACACCTCAGCAATGACCA 701
QY 491 CTGCGAGTATTTCTGTACAGATCTCTGCGGGGCTCAAGTACATCACTCGGCGAAGCT 550
DB 702 TATCTGCTATTTCTTACAGATCTCTCAGAGGTTAAATATATATCATTCAGCTAAGCT 761
QY 551 GATCCACCGGACCTGAAGCGGAGCAACCTGCTGCTGAAGCCCACTGCGACCTCAAGAT 610
DB 762 TCTGCACCGTGACCTCAAGCTTCCAACTGCTGCTCAACACCACTGCTGATCTCAAGAT 821
QY 611 CTGCGACTTCGGGCTGCGCGCGCGCTC-----GTCCGAGAGCGACATGATGAC 658

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DB 822 CTGTGACTTTGGCTGGCCCGGTGTTCCAGATCCAGACCATGATCACACAGGGTTCCTGAC 881
QY 659 GGAGTACGTGTGTCACCCGGTGTGTACCGCGCGCGGAGCTGTGCTCACTCCACCGACTA 718
DB 882 AGAATATGTGGCCACACACGTGGTGTACAGGGCTCCAGAAATTTATGTTGAAATTCGAAGGCTA 941
QY 719 CTCGGCGGCATCGAGCTGCTGGTCCGTGCGCTGCTGCTTTCATGAGAGCTCATCAACCGCCA 778
DB 942 CACCAAGTCCATGATATTTGGTCTGTAGGCTGCTTTCGGCAGAAATGCTTTTCCAAACAG 1001
QY 779 GCGGCTCTTCCCGCGGAGGAGCCACATGACACAGATGCGCCTCATCAGGAGTGTATCGG 838
DB 1002 GCCCATCTTTCCAGGAGACATTTATCTTGACCGAGCTGAATCACATTTTGGGTATTTCTGG 1061
QY 839 GAGCGGAGGAGCAGAGCTGGGTTCATACGGAACAGGAGCGGAGGAGTACATGAG 898
DB 1062 ATCCCCATCACAGAAGACCTGAAATTTGTAATAATAATTTAAAGAGCTAGGAACCTATTGCT 1121
QY 899 GCACCTGCGCGAGTACCCCGCGGAGCTTTCGCGAGCATGTTCCCGCGGTGCGAGCCGCG 958
DB 1122 TTCTCTTCCACACAAATAAAGTGCCATGGAACAGGCTGTTCCCAATGCTGACTCCAA 1181
QY 959 CGGCTCGACCTCATCGAGAGGATGCTCACCTTTCAACCGCTGCGAGAGATCAAGTTGA 1018
DB 1182 AGCTCTGAGCTTATTTGGACAAATGTTGACATTTCAACCCACACAGAGGATTTGAAGTAGA 1241
QY 1019 GAGGCGCTCGATCATCTTACCTAGAGATTTGACGACATCGCGAGTGGAGCCCATCTG 1078
DB 1242 ACAGGCTCTGGCCACCCATATCTGGAGCAGTATTACGAGCCGAGTGACGAGGCCATCGC 1301
QY 1079 CTTGGAGCCCTTCTCTCGACTTCGAGCAGAGGCTCTTAAACGAGGACCAATGAAGCA 1138
DB 1302 CGAAGCACCATTCAAGTTTGACATGGAATTTGGATGACTTGCCTTAAGGAAGCTAAAGA 1361
QY 1139 GCTGATCTTCAACGAAGCGATCGAGATGAACCCCAACATCCCGTACTAGATT 1190
DB 1362 ACTAATTTTGAAGAGACTGCTAGATTCCAGCCAGGATACAGATCTTAATTT 1413

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RESULT 4
US-10-909-125-861
; Sequence 861, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Beau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Koller, Eric
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Bigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; FILE REFERENCE: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 861

```


QY 739 GGTCCGTGGCTGCATCTTTCATGAGAGTCAATCAACCGCCAGCGCGTCTTCCCGGAGGG 798
|||
Db 1433 GGGGTGGGCTGCATCTTTCATGAGATGCCACAGGCGGTCCCTCTTTTCGGGGTCCA 1492
|||
QY 799 ACCACATGACACAGATGGCGCTCATCACGAGGTGATCGGAGCGCCGACGAGCGAGCG 858
|||
Db 1493 CGGTGAGGACACAGCTACACTTCTTTCGTTATCTTAGAAACCCCACTGAGGAGACT 1552
|||
QY 859 TGGGGTTTCATACAGAAACGAGGACGCGAGGAAGTACATGAGGCACCTTCGCGCATACCCGC 918
|||
Db 1553 GCGCAGGCATCTGTTCACACGAGGAGTTCAG--ACATACAACTACCCCAAGTACCGAG 1609
|||
QY 919 GCGGAGAGTTGCGGAGCATGTTCCCGGGGTGACGCCCGCGCGGTCTGACCTCATCGAGA 978
|||
Db 1610 CCGAGGCCCTTTTGAAGCCACGACCCCGACTTGTATAGCGACGGGGCCGACCTCTCACCA 1669
|||
QY 979 GGATGCTCACCTTCAACCCCGCTGCAGAGAAATCACAGTTGAGGAGGGCTCGATCATCCTT 1038
|||
Db 1670 AGCTGTTGAGTTTGAAGGTGGAATCGGATCTCCGACAGGATGCCATGAACATCCAT 1729
|||
QY 1039 ACCTAGAGAGATTGCACGA 1057
|||
Db 1730 TCTTCTCAGTCTGGGGA 1748
|||
RESULT 8
US-10-770-726-9
; Sequence 9, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 983
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-9

Query Match 9.2%; Score 128; DB 6; Length 983;
Best Local Similarity 50.6%; Pred. No. 3.4e-20;
Matches 429; Conservative 0; Mismatches 395; Indels 24; Gaps 4;

QY 201 ATTGGCCGGCGCGCTACGGGATCGTCTCGTGATGAACCTTTTGAGACGAGGAGATG 260
|||
Db 52 ATTGGGGAAGGCACCTACGGAACCTGTGTTCAAGGCCAAACCGGAGACTCATGATC 111
|||
QY 261 GTGGCGATTAAGAAGATCGCCAAACGGGTTCACACGACATGACGCCAAGCCAGCGCTC 320
|||
Db 112 GTGGCTCTGAACGGGTGGGCTGGATGACGATGAGGGTGTGCGGAGTTCCGCCCTC 171
|||
QY 321 CGGGAGATCAAGCTCTCAGGCACTCGACCGAGAACATCATAGGCATCAGGAGTNG 380
|||
Db 172 CGGGAGATCGCTTACTCAAGGAGCTGAAGCAACAGAACATCGTCAAGGCTTCATGACGTC 231
|||
QY 381 ATCCCGCCGCGATCCCTCAGGCGTTCAACGAGCTGTACATCGCCACGGAGCTCATGGAC 440
|||
Db 232 CTGCACAGCGACAAAGAGCTGACTTTGGTTTGAATTTCTGTACCGAGGACCTGAAGAG 291
|||
QY 441 ACCGACCTCCATCACAATCATTCGCTCAACCAAGAACTGTGAGAAGACACTGCCAGTAT 500
|||
Db 292 T-----ATTTTGACAGTTGCAATGGTGAACCTCGATCCTGAGATTGTAAAGTCA 339
|||
QY 501 TTCTCTTACAGATCTCGGGGGCTCAAGTATACATCCACTCGGCGAACTGATCCACCGC 560
|||
Db 340 TTCTCTTCCAGCTACTAAAGGGCTGGGATTCTGTATAGCGGCAATGTGTACTACAGG 399
|||

QY 561 GACCTGAAGCCGAGCAACTGCTGCTGAACCGCAACTCGCACTCAAGATCTGCGACTTC 620
|||
Db 400 GACCTGAAGCCCGACAGAACTGCTTAATAAACAGAAATGGGAGCTGAAATGGCTGATTT 459
|||
QY 621 GGGCTGGCGCGCGCTGCTCGGAGAGCGACATGA---TGACGAGTACGTGGTCAACCGG 677
|||
Db 460 GGCCTGGGTCGAGCCCTTTGGGATTCCTCCGCTTTACTCAGCTGAGGTGGTCACTG 519
|||
QY 678 TGGTACCGCGCGCGGAGCTGCTCAACTCCACCGACTACTCCGCGCGCACTCGACGTC 737
|||
Db 520 TGGTACCGCGCGCAACCGGATGCTCTTTTGGGGCCAAAGCTGTACTCACGTCATCGACATG 579
|||
QY 738 TGGTCCGTCGGTGCATCTTCATGAGACTCATCAACC---GCCAGCCGCTCTTCCCGGC 794
|||
Db 580 TGGTCAGCGCGCTGATCTTTTSCAGAGCTGGCAATGTGTGGCGGCGCTCTTTTTCGCGC 639
|||
QY 795 AGGAGACCATGACACAGATGGCCCTCATCACCAGGTGATCGGAGCGCGCGAGCGAC 854
|||
Db 640 AATGATGTGATGACCACTTGAAGAGGATCTTCCGACTGCTGGGACGCGCCACCGAGGAG 699
|||
QY 855 GAGCTGGGGTTTCATACCGAAACGAGGACGCGAGGAAGTACATGAGGCACCTGCGCGAGTAC 914
|||
Db 700 CAGTGGCCCTCTATGACCAAGCTGCAG-----ACTATAAGCCCTATCCGATGTACCCG 753
|||
QY 915 CCGCGCCGAGCGTTCCGAGCATGTTCCCGGGGTGACAGCCCGCGCTCGACCTCATC 974
|||
Db 754 GCCACAAACATCCTCGTGAAACGTCGTGCCCAAACCTCAATGCCACAGGAGGATCTGCTG 813
|||
QY 975 GAGAGATGCTCACCTTCAACCCGCTGCAGAGAAATCACAGTTGAGAGGCGCTCGATCAT 1034
|||
Db 814 CAGAACTTCTGAAGTGTAAACCTGTCCAGCGTATCTCAGCAGAAAGAGGCGCTCGAGCAC 873
|||
QY 1035 CCTTACCT 1042
|||
Db 874 CCTTACTT 881
|||
RESULT 9
US-10-770-726-7
; Sequence 7, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-7

Query Match 7.5%; Score 104.2; DB 6; Length 2328;
Best Local Similarity 48.6%; Pred. No. 1.2e-14;
Matches 413; Conservative 0; Mismatches 418; Indels 18; Gaps 4;

QY 201 ATTGGCCGGCGCGCTACGGGATCGTCTCGTGATGAACCTTTTGAGACGAGGAGATG 260
|||
Db 261 ATCGAGAGGCGACCTACGGAGTTGTATCAAGCCAGAAACAAGTTGACGGAGAGGTG 320
|||
QY 261 GTGGCGATAAAGAAGATCGCCAAACCGTTTCAACACGACATCGACCGCGACGCTC 320
|||
Db 321 GTGGCGCTTAAGAAATCGCGCTGACACTGAGACTGAGGGGTGTGCCAGTACTGCCATC 380
|||
QY 321 CGGAGATCAAGCTCTCAGGCACTCGACCGACCAACGAGAAATCATAGGCATCAGGATG 380
|||

Db 381 CGAGAGATCTCTGCTTAAAGAGCTTAACCATCTTAATATTTGTCAGAGCTGCTGGATGTC 440
 QY 381 ATCCCGCCGCGATCCCTCAGGCGTTCAACGAGCTTACATCGCCACGAGAGTCTATGGAC 440
 Db 441 ATTACACACAGAAATAAATCTACCTGGTTTTTGAATTTCTGCACCAAGATCTCAAGAAA 500
 QY 441 ACCGACTCCATCACATATCCGCTCAACCAAGAACTGTCAAGAGAGCACTGCCAGTAT 500
 Db 501 -----TTATGGATGCTCTGCTCTCAC--TGGAATTCCTTTCCCTCATCAAGAGC 551
 QY 501 TTCTCTACAGATCTCGGGGGGCTCAAGTACATCCACTCGGCGAAGCTGATCCACCGC 560
 Db 552 TATCTGTTCCAGCTGCTCAGGGCTAGCTTTCTGCCATTTCTCATCGGTTCTCCACCGA 611
 QY 561 GACCTGAAGCGAGCAACCTGCTGTGAAGCGCAACTGCGACCTCAAGATCTGCGACTTC 620
 Db 612 GACCTTAAACCTCAGAATCTGCTTATTAACACAGAGGGGGCCATCAAGCTAGCAGACTTT 671
 QY 621 GGGCTGGCGGCGGCTCGTGGAGAGCGACATGA---TGAAGAGTACGTGGTCAACCGG 677
 Db 672 GGAATGACAGAGCTTTTGGAGTCCCTGTTGCTACTTACACCCATGAGGTGGTGAACCTG 731
 QY 678 TGTACCGCGCGCGAGCTGCTGCTCAACTCCACCGACTACTCCGCGCCATCGACGTC 737
 Db 732 TGTACCGAGCTCTGAATCTCTCTGGGTGCAATATTTATTCACAGCTGTGGATC 791
 QY 738 TGTCTCGTGGCTGCTATCTTCAATGAGCTCATCAACCGCGAGCGCTCTTTCCCGCGAGG 797
 Db 792 TGGAGCTGGCTGCTATCTTTGCTGAGATGCTGACTCGCGGGCCCTATTTCCCTGGAGAT 851
 QY 798 GACCACATGACAGATGCGCTCATCACGAGTGTATGGGAGCGCGAGAGGAGG 857
 Db 852 TCTGAGATTTGACAGCTCTTTCGGATCTTTTCGGACTCTTGGGACCCCA-----GATGAG 905
 QY 858 CTGGGTTTATACGGAACGAGGAGCGGAGAGTACATGAGGCACTTCCCGCAGTACCCG 917
 Db 906 GTGGTGGCCAGAGTACTTCTATGCTGATTAAGCCAAATTTCCCAAGTGGGCC 965
 QY 918 CGCGGAGCTTCGCGAGCATGTTCCCGGGTGCAGCCCGCGCTCGACCTCATCGAG 977
 Db 966 CGGCAAGATTTTAAAGTTGTACTCCCTCGATGAGATGAGCGAGCTGTTTATCG 1025
 QY 978 AGATGCTACCTTCAACCGCTGCAGAGATCAGATTTGAGAGGGCTGATCATCT 1037
 Db 1026 CAAATGCTGACTACGACCCCTAAAGCGGATTTTCGGCAAGGAGCGCTGCTCACCT 1085
 QY 1038 TACTAGAG 1046
 Db 1086 TTCTTCAG 1094

RESULT 10

US-11-113-424-11
 ; Sequence 11, Application US/11113424
 ; Publication No. US20050260713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gangolli et al.
 ; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-225
 ; CURRENT APPLICATION NUMBER: US/11/113,424
 ; CURRENT FILING DATE: 2005-04-21
 ; PRIOR APPLICATION NUMBER: 60/256,704
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: 60/311,590
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/257,314
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: 60/311,613
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/315,617
 ; PRIOR FILING DATE: 2001-08-29
 ; PRIOR APPLICATION NUMBER: 60/307,506
 ; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358
 ; PRIOR FILING DATE: 2001-09-14
 ; PRIOR APPLICATION NUMBER: 60/294,075
 ; PRIOR FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: 60/288,153
 ; PRIOR FILING DATE: 2001-05-02
 ; NUMBER OF SEQ ID NOS: 190
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 3073
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-11-113-424-11

Query Match 6.8%; Score 95.6; DB 7; Length 3073;
 Best Local Similarity 48.8%; Pred. No. 1.2e-12;
 Matches 288; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
 QY 200 CATTGGCGCGCGCTACGGGATGCTGCTCGGTGATGAACCTTTGAGACGAGGAGAT 259
 Db 695 CATTGGCGCGCGGCTTTTGGCGAGTCTATGGGTCCCGAAGCGTGAACAGGCAAGAT 754
 QY 260 GGTGGCGATAAAGAGATCGCCAAACGCGTTCAACACAGCATGAGCGCCAAAGCGACGCT 319
 Db 755 GTACGCCATGAGTGCCTGACAAAAGCGCATCAAGATGAAGACGAGGAGACCTTGGC 814
 QY 320 CCGGAGAGATCAAGCTCTCAGGCACCTCGACCAACGAGAAATCATAGGATCAGGAGTGT 379
 Db 815 CTTGAACGAGCGCATCATGCTCTCGCTCAGCAGCTGGGAGCTGCCCATTTATTGTCTG 874
 QY 380 GATCCCGCGCGATCCCTCAGGCGTTCAACGAGCTTACATCGCCACGAGGCTCATGGA 439
 Db 875 CATGTACATACGCGTTCCACACGCCAGCAAGCTCAGCTTCATCTCGACCTCATGAACGG 934
 QY 440 CACCGACTCCCATCATCATATCCGCTCCAAACCAAGAACTGTTCAGAAAGAGCACTGCCAGTA 499
 Db 935 TGGGAGCTTGCATACCACTCTCCAGCAGCGGGTCTTTCAGAGGCTGACATGCGCTT 994
 QY 500 TTTCTGTATACAGATCCTCGGGGGCTCAAGTATACATCCACTCGGCGAAACGTGATCCACCG 559
 Db 995 CTATGCGCGCGAGATCATCTCGGGCTGGAGCAGATGCAACCCGCTTCGTGTCTACCG 1054
 QY 560 CGACCTGAAGCGGAGCAACCTGCTGCTGAACGCCCACTCGACCTCAAGATCTGCGACTT 619
 Db 1055 GGACCTGAAGCCAGCAGCAATCTTCTTGACAGCATGCGCACGCGGATCTCGGACCT 1114
 QY 620 CGGGCTGGCGCGCGCTCGTCCGAGAGCGACATGATGACGAGTAGTGTGTCACCGGTG 679
 Db 1115 GGGCTGGCTGTGACTTCTCCAGA---AGAGCCCCATGCCAGGCTGGGACCCACGG 1171
 QY 680 GTACCGCGCGCGAGCTGCTGCTCAACTCCACCGACTACTCCGCGCCCATCGAGCTGTG 739
 Db 1172 GTACATGGCTCCGAGGCTCTCGAGAAGGCGGTGGGCTAGCAGACAGTAGTCCGACTGTT 1231
 QY 740 GTCCGTGCGTGCATCTTTCATGAGGCTCATCAACCCGAGCGCTTCTTCC 789
 Db 1232 CTCTCTGGGGTGCATGCTCTTCAAGTTGCTGGCGGGGACAGCCCTTCC 1281

RESULT 11

US-10-750-185-28925/c
 ; Sequence 28925, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2

```
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28925
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Bovine 19866881174740
US-10-750-185-28925

Query Match      6.6%; Score 92; DB 6; Length 1400;
Best Local Similarity 56.9%; Pred. No. 6.2e-12;
Matches 189; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

QY 496 AGTATTTCCTGTACCAAGATCTCGCGGGGCTCAAGTACATCCACTCGCGGAAGTGATCC 555
DB 730 AGAGCTACTTGTTCAGCTGTCTCCAGGCGCTCACTTTCTGCCACTCTCATTTGGGTCTGC 671
QY 556 ACCGCGACCTGAAAGCCGAGCAACCTGCTGCTGAACGCCAACTGCGGACCTCAAGATCTGCG 615
DB 670 ACCGAGACCTCAAACTCTAGATCTGCTTATCAACGCAGATGGGTCCATCAAGCTAGCAG 611
QY 616 ACTTCGGGTGGCGCGCGCTGCTCGAGAGCG---ACATGATGACGGAGTAGTGCTCA 672
DB 610 ACTTCGGGACTAGCCAGAGCTTTTGGGGTCCCTTTTCATATCTTATACCGACGAGGTGGTGA 551
QY 673 CCGGGTGGTACCGCGCGGAGCTGCTGCTCAACTCCACCGACTACTCGCGGCCATCG 732
DB 550 CTCGTGGTACTGAGCACTGGAATCTTCTGGGCTGCAAACTACTCTCATAGCTGTGG 491
QY 733 ACCTCTGGTCCGTCGGCTGTCATCTTCATGAGCTCATCAACCGCCAGCGGCTCTTCCCG 792
DB 490 ACATCTGGAGCTCGGTGTCATCTTTGCTGAGATGGTACCCTGCGGCGCTATTCTCTG 431
QY 793 GCAGGACCAACATGCAACCGATCGGCTCATC 824
DB 430 GAGACTCTGAGATCAACCAACTCTCCAGATC 399

RESULT 12
US-10-770-726-8
; Sequence 8, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-8

Query Match      5.4%; Score 75.8; DB 6; Length 1474;
Best Local Similarity 51.4%; Pred. No. 3.1e-08;
Matches 201; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

QY 466 CCAACCAAGACTGTGAGAGAGCACTGCCAGTATTTCTGTACCAAGATCTTCGCGGGGC 525
DB 550 CCCACCAAGCTTGCAGCGGAAACGATCAAGATCTGATGCGCCAGTTTCTAAGAGGCC 609
QY 526 TCAAGTACATCCACTCGCGGAAGCTGATCCACCGGACCTGAAGCCGAGCACTGCTGCG 585
DB 610 TAGATTCTTTCATGCAATTGATCGTTCAACCGAGATCTGAAGCCAGAGAACATTTCTGG 669
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QY 586 TGAACGCCAACTGCGACCTCAAGATCTCGCACTTCGGGCTGCGCGCGCTCGTCGGAGA 645
DB 670 TGAACAAGTGGTGAACACAGTCAAGCTGGCTGACTTTTGGCTGGCCAGAAATCTACAGTACC 729
QY 646 GCGACATGATGACGGAGTACGTGGTCAACCCGGTGTACCGCGCGCGGAGCTGCTGCTCA 705
DB 730 AGATGGCACTTACACCCCGTGTGTACACTCTGTGTACCGAGCTCCCGAAGTTCTTCTGC 789
QY 706 ACTCCACCGACTACTCCGCGGCATCGACGCTGTGGTCCGTCCGTGCTGTCATCTTTCATGGAGC 765
DB 790 AGTCCAC---ATATGCAACACCTGTGACATGTGAGTGTGGCTGTATCTTTGCAGAGA 846
QY 766 TCATCAACCGCCAGCCGCTCTTCCCGCGCAGGACACATGCACAGATGCGCCTCATCA 825
DB 847 TGTTTTCGTCGAAAGCTCTCTTCTGTGAAACTCTGAAAGCCGACCAAGTTGGGCAAAATCT 906
QY 826 CCGAGGTGATCGGAGCGCGGACGAGCAGCA 856
DB 907 TTGACCTGATTGGGCTGCTCCAGAGGATGA 937

RESULT 13
US-10-770-726-27
; Sequence 27, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

Query Match      4.6%; Score 63.6; DB 6; Length 2838;
Best Local Similarity 47.7%; Pred. No. 2.3e-05;
Matches 186; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 399 CAGGCGTTCAACGACGTCTACATCCACCGAGAGCTATGCCACGAGCTCATGGACACCGACTCCATCATC 458
DB 1366 CTGGTGGGGGACGAGCTCTGGGTGGTCTATGGAGTTCTTGGAGAGGCGCCCTCACCGAC 1425
QY 459 ATCCGCTCCAAACCAAGAACTGTCAAGAGACACTGCCAGTATTTCTGTACCAGATCCCTG 518
DB 1426 ATCGTCAACCAACCCAGGATGAACGAGGAGCAGATCGCGCGCTGTGCTTGCAGTGTCTG 1485
QY 519 CGGGGGCTCAAGTATCATCCACTCGCGGAACTGTGATCCACCGGAGCTCTGAAGCCGAGCAAC 578
DB 1486 CAGGCGCTGTGGTCTCCACCGCCCGGCGTCTATCCACCGGAGATCAAGAGCGACTCG 1545
QY 579 CTGCTGTGAAGCCCACTCGGACCTCAAGATCTCGGACTTCGGGCTGCGCGCGCGGCTCG 638
DB 1546 ATCTCTGTGACCCATGATGCGAGGGTGAAGCTGTGAGACTTTTGGGTCTTGGCGCCAGG 1605
QY 639 TCGGAGAGCGACATGATGACGAGTACGTGGTGTACCCCGTGTATCCGCGCGCGGAGCTG 698
DB 1606 AGCAAGGAGTGCCTCCGGAAGGATGCTGTGTGGACAGCCCTATGTGATGCGCCCGAG 1665
QY 699 CTGCTCAATCCACCGACTACTCCCGCGCATTCGACGTCTGCTCGCTCGGCTGCAATCTTC 758
DB 1666 CTCTCTCCCGCTTCTCCCTACGGGCGAGAGGTAGACATCTGCTGCTGGGATATGCTG 1725
QY 759 ATGGAGCTCATCAACCGCGAGCGCTCTTC 788
```

Db 1726 ATTGAGATGGTGGACGGAGGCCCCCTAC 1755

RESULT 14

US-10-750-185-35100

; Sequence 35100, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35100

; LENGTH: 2497

; TYPE: DNA

; ORGANISM: Bovine 19866881358776

US-10-750-185-35100

Query Match 4.5%; Score 63; DB 6; Length 2497;

Best Local Similarity 55.0%; Pred. No. 3e-05;

Matches 93; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 561 GACCTGAAGCCGAGCAACCTGCTGCTGAACGCCAAGCTCGACCTCAAGATCTGCGACTTC 620

Db 1338 GATCTGAGCCCTAGTAACTTGTAGTAAAGTCAGACTGCACCTGAAGATCTCTCGACTTT 1397

QY 621 GGCTGGCGGGCGCTGCTGGAGAGGACATGATGACGGAGTACGTGTCACCCGGTGG 680

Db 1398 GGCTGGCTGCTACAGCGTGACCAACTTTATGATGACTCCCTATGCTGCTCACCGTAT 1457

QY 681 TACCGGCGCGCGAGCTGCTGCT 703

Db 1458 TACCGGCGACCTGAAAGTCAFCCT 1480

Db 1726 ATTGAGATGGTGGACGGAGGCCCCCTAC 1755

RESULT 15

US-10-770-726-35

; Sequence 35, Application US/10770726

; Publication No. US20050286409A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Brown, Eugene

; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

; FILE REFERENCE: AM101079 (031896-010000)

; CURRENT APPLICATION NUMBER: US/10/770,726

; CURRENT FILING DATE: 2004-02-04

; NUMBER OF SEQ ID NOS: 48640

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 35

; LENGTH: 3527

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-770-726-35

Query Match 4.3%; Score 60.4; DB 6; Length 3527;

Best Local Similarity 46.9%; Pred. No. 0.00013;

Matches 227; Conservative 0; Mismatches 251; Indels 6; Gaps 1;

QY 292 ACAACGACATGGAGCCAGCGACGCTCCGGGAGATCAAGCTCCTCAGGACACTCGACC 351

Search completed: December 29, 2005, 08:06:46

Job time : 198 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:36:37 ; Search time 13 Seconds
(without alignments)
201.913 Million cell updates/sec

Title: US-10-768-886-2
Perfect score: 1953
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DOMKQLIFNEAITEMPNTRY 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	887	45.4	379	7	US-11-109-156-16
2	878	45.0	360	6	US-10-878-556A-134
3	878	45.0	360	7	US-11-186-284-115
4	747.5	38.3	365	6	US-10-770-726-69
5	653	33.4	422	6	US-10-857-780-21
6	518	26.5	422	6	US-10-770-726-53
7	491.5	25.2	496	6	US-10-770-726-72
8	467.5	23.9	298	6	US-10-770-726-51
9	461	23.6	346	6	US-10-770-726-55
10	457	23.4	297	6	US-10-770-726-48
11	457	23.4	297	7	US-11-109-156-11
12	440	22.5	433	6	US-10-770-726-65
13	438	22.4	483	6	US-10-451-375-12
14	435.5	22.3	795	6	US-10-770-726-49
15	434.5	22.2	303	6	US-10-770-726-52
16	433	22.2	256	7	US-11-113-424-183
17	349.5	17.9	391	6	US-10-770-726-59
18	321.5	16.5	355	6	US-10-451-375-2
19	321.5	16.5	457	6	US-10-451-375-6
20	313.5	16.1	1162	6	US-10-451-375-3
21	312.5	16.0	1198	6	US-10-451-375-4
22	305	15.6	333	7	US-11-004-789-2
23	305	15.6	334	7	US-11-111-239-4
24	296	15.2	318	7	US-11-109-156-15
25	296	15.2	1133	6	US-10-821-234-1219

26	295.5	15.1	318	7	US-11-111-239-2	Sequence 2, Appli
27	286	14.6	970	6	US-10-770-726-86	Sequence 86, Appl
28	279	14.3	275	6	US-10-523-477-10	Sequence 10, Appl
29	277.5	14.2	603	6	US-10-770-726-75	Sequence 75, Appl
30	274	14.0	433	7	US-11-109-156-9	Sequence 9, Appli
31	273	14.0	591	6	US-10-770-726-71	Sequence 71, Appl
32	271.5	13.9	403	6	US-10-523-477-11	Sequence 11, Appl
33	271.5	13.9	403	6	US-10-770-726-83	Sequence 83, Appl
34	271.5	13.9	403	6	US-10-770-726-85	Sequence 85, Appl
35	271.5	13.9	403	7	US-11-109-156-12	Sequence 12, Appl
36	271.5	13.9	403	7	US-11-092-168-1	Sequence 2, Appli
37	270	13.8	540	7	US-11-099-691-2	Sequence 2, Appli
38	269.5	13.8	766	6	US-10-821-234-1691	Sequence 1691, Ap
39	268.5	13.7	651	6	US-10-770-726-67	Sequence 67, Appl
40	266.5	13.6	471	6	US-10-770-726-68	Sequence 68, Appl
41	263.5	13.5	740	6	US-10-878-556A-129	Sequence 129, App
42	263	13.5	332	6	US-10-497-767-3	Sequence 3, Appli
43	260	13.3	348	6	US-10-661-426-12	Sequence 12, Appl
44	256	13.1	445	6	US-10-770-726-70	Sequence 70, Appl
45	255.5	13.1	366	6	US-10-661-426-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-11-109-156-16
; Sequence 16, Application US/1109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-16

Query Match 45.4%; Score 887; DB 7; Length 379;
Best Local Similarity 50.0%; Pred. No. 4.6e-70;
Matches 173; Conservative 65; Mismatches 100; Indels 8; Gaps 5;

QY 26 GNKFEVTKYQPPIMPGRGAYGIVCSVMNFETREMAVKKIANAFNNDMDAKRTILREIK 85
DB 33 GQPFVDPGRY-TOLQVIGEGAYGMVSSAYDNVNRKTRVAIKKI-SPEHQTYCQRTILREIQ 90
QY 86 LLRHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTLHIIIRSNQELSEBHCQVFLYQ 145
DB 91 LLRFRHENIIGIRDVIRASTLEAMRDVYIVQDLMETDLYKLLKS-QQLSNDHICVFLYQ 149
QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLAR-----PSESDDMTTEYVYVTRW 201
DB 150 ILRGLKYIHSANVHRDLKPSNLLNTTCDLKICDFGLARIADPEHDHTGFLTEYVYVTRW 209
QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFPGRDHMHQMLITEVIGTPTDDEL 260
DB 210 YRAPEIMLNSKGYTSIDISWVGCILAEMLSNRPIPPGKHLYDQLNHLILGILGSPSQEDL 269
QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTIVVEALDHPY 320
DB 270 NCIIINKARNYLOSLSKTKVAWKLFPKSDSKALDLDLDRMLTFNPKRTIVVEALAHFY 329
QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEKNPNIR 366
DB 330 LEQYYDPTDEPVAEEPTFAMELDDLPKEKLKELIFEETARFQPGV 375

RESULT 2

US-10-878-556A-134
; Sequence 134, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/mk01_human
; DATABASE ENTRY DATE: 1992-12-01
US-10-878-556A-134

Query Match 45.0%; Score 878; DB 6; Length 360;
Best Local Similarity 50.1%; Pred. No. 2.6e-69;
Matches 174; Conservative 61; Mismatches 104; Indels 8; Gaps 5;

QY 26 GNKFEVTKYQPPIMPGRGAYGIVCSVMNFETREMAVKKIANAFNNDMDAKRTILREIK 85
DB 16 GQPFVDPGRY-TNLSYIGEGAYGMVCSAYDNVNRKTRVAIKKI-SPEHQTYCQRTILREIK 73
QY 86 LLRHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTLHIIIRSNQELSEBHCQVFLYQ 145
DB 74 LLRFRHENIIGINDIRAPTIQOMKDVYIVQDLMETDLYKLLKT-QHLSNDHICVFLYQ 132
QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS-----SSEDDMTTEYVYVTRW 201
DB 133 ILRGLKYIHSANVHRDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVYVTRW 192
QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFPGRDHMHQMLITEVIGTPTDDEL 260
DB 74 LLRFRHENIIGINDIRAPTIQOMKDVYIVQDLMETDLYKLLKT-QHLSNDHICVFLYQ 132
QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS-----SSEDDMTTEYVYVTRW 201
DB 133 ILRGLKYIHSANVHRDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVYVTRW 192
QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFPGRDHMHQMLITEVIGTPTDDEL 260
DB 193 YRAPEIMLNSKGYTSIDISWVGCILAEMLSNRPIPPGKHLYDQLNHLILGILGSPSQEDL 252
QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTIVVEALDHPY 320
DB 253 NCIIINKARNYLOSLSKTKVAWKLFPKSDSKALDLDLDRMLTFNPKRTIVVEALAHFY 312

QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEKNPNIR 367
DB 313 LEQYYDPSDEPTAEAPFFKDFMELDDLPKEKLKELIFEETARFQPGV 359

RESULT 3

US-11-186-284-115
; Sequence 115, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-0292P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-115

Query Match 45.0%; Score 878; DB 7; Length 360;
Best Local Similarity 50.1%; Pred. No. 2.6e-69;
Matches 174; Conservative 61; Mismatches 104; Indels 8; Gaps 5;

QY 26 GNKFEVTKYQPPIMPGRGAYGIVCSVMNFETREMAVKKIANAFNNDMDAKRTILREIK 85
DB 16 GQPFVDPGRY-TNLSYIGEGAYGMVCSAYDNVNRKTRVAIKKI-SPEHQTYCQRTILREIK 73
QY 86 LLRHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTLHIIIRSNQELSEBHCQVFLYQ 145
DB 74 LLRFRHENIIGINDIRAPTIQOMKDVYIVQDLMETDLYKLLKT-QHLSNDHICVFLYQ 132
QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS-----SSEDDMTTEYVYVTRW 201
DB 133 ILRGLKYIHSANVHRDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVYVTRW 192
QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFPGRDHMHQMLITEVIGTPTDDEL 260
DB 193 YRAPEIMLNSKGYTSIDISWVGCILAEMLSNRPIPPGKHLYDQLNHLILGILGSPSQEDL 252
QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTIVVEALDHPY 320
DB 253 NCIIINKARNYLOSLSKTKVAWKLFPKSDSKALDLDLDRMLTFNPKRTIVVEALAHFY 312
QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEKNPNIR 367
DB 313 LEQYYDPSDEPTAEAPFFKDFMELDDLPKEKLKELIFEETARFQPGV 359

RESULT 4

US-10-770-726-69
; Sequence 69, Application US/10770726

```
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 365
; TYPE: PR
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-770-726-69
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Query Match 38.3%; Score 747.5; DB 6; Length 365;
Best Local Similarity 43.2%; Pred. No. 5.9e-58;
Matches 150; Conservative 65; Mismatches 125; Indels 7; Gaps 5;

QY 23 DIFGNKFEVNTKYQPPIMPGRGAGIVCSVMNPFETREMAIKKIANAFNNDMDAKRTLR 82
DB 13 DVNKTAWELPKTVSP-THVSGGAGYSCSAIDKRSGEKVAIKLSRPFQSEIFAKRAYR 71
QY 83 EIKLLRHLDHENTIIGIRDVIPP-PAFNDVVIATLMDTDLHHIIRSNQELSEHCQY 141
DB 72 ELALLKHEQHEWIGLLDVFTPASSLRNFYDFYLVMPFMQTDLQKIM--QWEPSEKIQY 129
QY 142 FLYQILRLGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPSSESDMTTEYVYVTRW 201
DB 130 LVYQMLKGLKYIHSAGVYVHRDLKPSNLLNANCDLKICDFGLARHADAE--MTGYVYVTRW 187
QY 202 YRAPELLNSTDYS--AADVMSVGCIFMELNROPLPGRDHMHQMLRITVIGTPTDDEL 260
DB 188 YRAPEVILSMWYNTQVDSVSGCIMAEMTGKILFKGKYLDQLTQLKVTGVPGETFV 247
QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTVBEALDHPY 320
DB 248 QKLNDKAASYIQSLQTPKDFQFLPFRASQQAADLERQWLELDVDRKLTAAQALTHFP 307
QY 321 LERLHDIADEPICLEPSPFBEQKALNEDQKQLIFNEALEMPNIR 367
DB 308 FEPFRDPEETEQAQPPDDSLSEHEKLTVDWKHYKEIYNFSPAR 354
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```
RESULT 5
US-10-857-780-21
; Sequence 21, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 422
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; TYPE: PR
; ORGANISM: Homo sapiens
US-10-857-780-21
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Query Match 33.4%; Score 653; DB 6; Length 422;
Best Local Similarity 40.5%; Pred. No. 1.2e-49;
Matches 145; Conservative 68; Mismatches 115; Indels 30; Gaps 10;

QY 23 DIFGNKFEVNTKYQPPIMPGRGAGIVCSVMNPFETREMAIKKIANAFNNDMDAKRTLR 82
DB 52 EVGDSFTVTLKRYQ-NLKPIGSAQOQIVCAAYDAVLDRNVAIKLSRPFQNOHTAKRAYR 110
QY 83 EIKLLRHLDHENTIIGIRDVI-PPPIPOAFNDVVIATLMDTDLHHIIRSNQELSEHCQY 141
DB 111 ELVLMKCVNHNKIISLVNFTFQKLESEFQDLYLWELMDANLCQVIQ--MELDHERMSY 168
QY 142 FLYQILRLGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPSSESDMTTEYVYVTRW 201
DB 169 LLYQMLCGIKHLHSAGIHRDLKPSNIVVKSDDCTLKILDFGLARTAGTSFMMTPYVYVTRY 228
QY 202 YRAPELLNSTDYSAADVMSVGCIFMELNROPLPGRDHMHQMLRITVIGTPTDDELG 261
DB 229 YRAPEVILMGYKENVDIWSVGCIMGEMVRHKILPFGDYIDQWNVIBQLGTPCPPE--- 285
QY 262 FIR--NEDARKYMRHLPOYPRRTFASMP- RVQPA-----ALDLIERMLTFNPL 307
DB 286 FMKQLOPTVRNVYENRPKYAGLTFPKLFPDSLFPADSEHNKLSKASQARDLLSKQLVIDPA 345
QY 308 QRTVBEALDHPYLERLHDIADEPICLEPSPFBEQKALNE-----DOMKQLIFNEAI 360
DB 346 KRISVDALQHPYINWYDPA-EVEAPPQIYD---KOLDEREHTIEENKELIYKEVM 399
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```
RESULT 6
US-10-770-726-53
; Sequence 53, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 292
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-770-726-53
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```
Query Match 26.5%; Score 518; DB 6; Length 292;
Best Local Similarity 40.0%; Pred. No. 3.9e-38;
Matches 120; Conservative 52; Mismatches 98; Indels 30; Gaps 10;

QY 34 KYOPPTMPIGRGAGIVCSVMNPFETREMAIKKIANAFNNDMDAKRTLRILKILRLHDHE 93
DB 3 KYE-KLEKIGEGYGVTFKAKNRETHEIVALKRVLDDDDDEGVPSALREICLLKELKH 61
QY 94 NIIGIRDVIPPPIPOAFNDVVIATLMDTDLHHIIRSNQELSEHCQYFLYQILRLGLKY 152
DB 62 NIVRLHDVL-----HSDKKLTLPFCQDLKKYFDCSCNGDLDPKVFLLKGLGF 116
QY 153 IHSANVHRDLKPSNLLNANCDLKICDFGLARP-----SSESDMTTEYVYVTRVRA 204
DB 117 CHSRNVLRDLKPSNLLNANCDLKICDFGLARP-----SSESDMTTEYVYVTRVRA 169
QY 205 PELLNSTDYSAA--DVMSVGCIFMELNROPLPGRDHMHQMLRITVIGTPTDDEL-G 261
DB 170 PDVLFKGLYSTDWMSAGCIFAELANAGRPLPFGNDVDDQLKRIPLILGTPTEEQWPS 229
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; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-11

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Query Match	23.4%;	Score 457;	DB 7;	Length 297;
Best Local Similarity	36.1%;	Pred. No. 8e-33;		
Matches	105;	Conservative 54;	Mismatches 120;	Gaps 12; Indels 5;

Qy	39	IMPIGAGATVCSVNVPETREMWVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIGI	98
Dd		: : : : : : : : : : : : : : : : : : : :	
	7	IEKIGBTGVWYKGRHKTGGVAMKKIRLESEEGVPSATAIREISLLKELRHPNVSL	66
Qy	99	ROVIPPPIQAFNDVVIATELMDTDLHLHIIRS--NQELSEHCQFYQLRLGLKYTHS	155
Dd	67	QDVL-----MQDSRLYLIIPEFLSSMDLUKXYLDSIPPGQYMS:: : : : : :	121
Qy	156	ANVTHRDLKPSNILLNANCCLKICDFGLARP-SSESDMTEYVVTRWYRAPELLINSTDY	214
Dd	122	RRVLRHDLKPQNLLIDDKTGFIKLADFGLARAFGIPRVYTHEVTLWYRSPEVLGSARY	181
Qy	215	SA-ADVWSVCIFPWEILINRQPLFPGRDHHQMBLITEVICPTDDLEGFINNEDARKYMR	273
Dd	182	STPDVDSWISGTIFAELATKKPLFGHDSEIDQLPRIFRALCTPNNEWNPVEV--ESLQDYKN	239
Qy	274	HLPQYPRRTFASMPRPVQAALDIIRMULTFNPLQRITVEEALDHPYLERL	324
Dd	240	TFPKWTPGSLASHVGNLDENGDLLSKMLTYDPAKRISGRWALNHYPFNDL	290

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RESULT 12
US-10-770-726-65
; Sequence 65, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-65

Query Match      22.5%; Score 440; DB 6; Length 433;
Best Local Similarity 31.3%; Pred. No. 3.9e-31;
Matches 103; Conservative 53; Mismatches 97; Indels 76; Gaps 8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:33:21 ; Search time 164 Seconds
(without alignments)
937.568 Million cell updates/sec

Title: US-10-768-886-2
Perfect score: 1953
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DQMKQLIFNEAEMPNIRY 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1953	100.0	368	4	US-10-768-886-2
2	1819.5	93.2	369	5	US-10-732-923-1342
3	1775.5	90.9	397	4	US-10-425-115-191397
4	1682.5	86.1	374	4	US-10-767-701-45777
5	1476.5	75.6	376	5	US-10-732-923-1332
6	1461.5	74.8	375	5	US-10-732-923-1324
7	1448.5	74.2	396	5	US-10-732-923-1446
8	1437.5	73.6	394	5	US-10-732-923-1447
9	1436.5	73.6	393	5	US-10-732-923-1331
10	1430	73.2	365	5	US-10-732-923-1334
11	1421.5	72.8	394	5	US-10-732-923-1323
12	1340.5	68.6	318	4	US-10-424-599-284784
13	1340.5	68.6	318	4	US-10-425-114-49119
14	1334.5	68.3	266	4	US-10-768-886-4
15	1331.5	68.2	377	4	US-10-767-701-45781
16	1331.5	68.2	403	4	US-10-425-114-67488
17	1325.5	67.9	372	4	US-10-425-115-271614
18	1325.5	67.9	380	4	US-10-425-114-67200
19	1323	67.7	395	4	US-10-437-963-137817
20	1322.5	67.7	376	4	US-10-437-963-139244
21	1316.5	67.4	376	3	US-09-730-478A-2
22	1310.5	67.1	417	5	US-10-732-923-1280
23	1295.5	66.3	379	5	US-10-732-923-1448
24	1260.5	64.5	375	3	US-09-828-313-34
25	1260.5	64.5	375	4	US-10-768-863A-34
26	1232.5	63.1	373	5	US-10-739-930-10557
27	1090.5	55.8	295	4	US-10-767-701-43229

28	1074.5	55.0	216	4	US-10-425-114-42499	Sequence 42499, A
29	1012	51.8	369	4	US-10-767-701-42772	Sequence 42772, A
30	1003.5	51.4	370	5	US-10-739-930-10966	Sequence 10966, A
31	995	50.9	370	4	US-10-767-701-45385	Sequence 45385, A
32	993	50.8	247	4	US-10-425-114-55085	Sequence 55085, A
33	987.5	50.6	372	4	US-10-425-114-62386	Sequence 62386, A
34	985.5	50.5	480	4	US-10-168-844-9	Sequence 9, Appli
35	985	50.4	368	5	US-10-732-923-1302	Sequence 1302, Ap
36	982	50.3	370	4	US-10-342-224-104	Sequence 104, App
37	981	50.2	368	5	US-10-739-930-6166	Sequence 6166, Ap
38	965	49.4	369	4	US-10-424-599-177815	Sequence 177815,
39	949.5	48.6	227	4	US-10-424-599-284783	Sequence 284783,
40	933.5	47.8	354	5	US-10-732-923-1366	Sequence 1366, Ap
41	932	47.7	371	5	US-10-739-930-10965	Sequence 10965, A
42	929	47.6	371	4	US-10-424-599-206406	Sequence 206406,
43	927	47.5	353	5	US-10-732-923-1492	Sequence 1492, Ap
44	926.5	47.4	261	4	US-10-425-115-350696	Sequence 350696,
45	925.5	47.4	308	4	US-10-425-115-350699	Sequence 350699,

ALIGNMENTS

RESULT 1
US-10-768-886-2
; Sequence 2, Application US/10768886
; Publication No. US20040209325A1
; GENERAL INFORMATION:
; APPLICANT: Board of Trustees for University of Arkansas
; TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance
; TITLE OF INVENTION: Biotic and Abiotic Stress Tolerance in Plants
; FILE REFERENCE: UAP-03-14
; CURRENT APPLICATION NUMBER: US/10/768,886
; CURRENT FILING DATE: 2004-01-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-768-886-2

Query Match	100.0%;	Score 1953;	DB 4;	Length 368;
Best Local Similarity	100.0%;	Pred. No. 7.1e-153;		
Matches 368;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDGAPVAEPRPTWTHGGRYLLYDI	FGNKPRTVKYOPPIMPICRGAYGIVCSVMNFETRE	60
DB	1	MDGAPVAEPRPTWTHGGRYLLYDI	FGNKPRTVKYOPPIMPICRGAYGIVCSVMNFETRE	60
QY	61	MVAIKKIANAFNNDMAKRTLRKILRLHLDHNIIGIRDVIPPPIPOAFNDVYIATELM	120	
DB	61	MVAIKKIANAFNNDMAKRTLRKILRLHLDHNIIGIRDVIPPPIPOAFNDVYIATELM	120	
QY	121	DTDLHHIIRSNQELSEHCQFLYQLRGKYTHSANVHRDLKPSNLLNANCDLKICD	180	
DB	121	DTDLHHIIRSNQELSEHCQFLYQLRGKYTHSANVHRDLKPSNLLNANCDLKICD	180	
QY	181	FGLARPSSESDMMTEVTVTRWRAPELLNSTDYSAADVMSVGCIFMELINRQPLPFGRD	240	
DB	181	FGLARPSSESDMMTEVTVTRWRAPELLNSTDYSAADVMSVGCIFMELINRQPLPFGRD	240	
QY	241	HMHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDLIER	300	
DB	241	HMHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDLIER	300	
QY	301	MLTFNPLQRIITVEALDHPYLRHLDADEPICLEPSPDFEQKALNEDQMKLIIFNEAI	360	
DB	301	MLTFNPLQRIITVEALDHPYLRHLDADEPICLEPSPDFEQKALNEDQMKLIIFNEAI	360	
QY	361	EMNPRIY 368		
DB	361	EMNPRIY 368		

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RESULT 2
US-10-732-923-1342
; Sequence 1342, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1342
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Avena sativa
US-10-732-923-1342

Query Match      93.2%; Score 1819.5; DB 5; Length 369;
Best Local Similarity 91.3%; Pred. No. 7.5e-142;
Matches 337; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDGAPVAEPRPTMTGGRFLYNYIFGNQFEITSKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 DTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVTHRDLPKSNLLNANCDLKICD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVTHRDLPKSNLLNANCDLKICD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FGLARPSSESDMTTEYVTRWYRAPELLLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FGLARPSSESDMTTEYVTRWYRAPELLLNSTDYSAAIDVMSVGCIFMELINRQPLFPGR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 RMLTFNPLQRTITVEEALDHPYLRHLHDADEP 331
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 RMLTFNPLQRTITVTVRHEWHGGRFRPRTSHRDLFCHAVAEALAHPLYERLHDVDDDEP 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FGLARPSSESDMTTEYVTRWYRAPELLLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FGLARPSSESDMTTEYVTRWYRAPELLLNSTDYSAAIDVMSVGCIFMELINRQPLFPGR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 RMLTFNPLQRTITVEEALDHPYLRHLHDADEP 331
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 RMLTFNPLQRTITVTVRHEWHGGRFRPRTSHRDLFCHAVAEALAHPLYERLHDVDDDEP 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 332 ICLEPFESDFEQKALNEDQMKQLIFNEAIEKMPNIRY 368
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 VCTEFESDFEQKALNEDQMKQLIFNEAIEKMPNIRY 397
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RESULT 3
US-10-425-115-191397
; Sequence 191397, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 191397
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Zea mays

Query Match      86.1%; Score 1682.5; DB 4; Length 374;
Best Local Similarity 87.3%; Pred. No. 1.6e-130;
Matches 322; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 MDGAPVAEPRPTVTHNGFLQYINIFGNLFEITHKYQPPIMPPIGRGAYGIVCSVMNFETRE 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(397)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106134C.1.pep
US-10-425-115-191397

Query Match      90.9%; Score 1775.5; DB 4; Length 397;
Best Local Similarity 84.4%; Pred. No. 3.5e-138;
Matches 335; Conservative 20; Mismatches 13; Indels 29; Gaps 2;

QY 1 MDGAPVAEPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDGAPVAEPRPTMTGGRFLYNYIFGNQFEITAKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 DTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVTHRDLPKSNLLNANCDLKICD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVTHRDLPKSNLLNANCDLKICD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FGLARPSSESDMTTEYVTRWYRAPELLLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FGLARPSSESDMTTEYVTRWYRAPELLLNSTDYSAAIDVMSVGCIFMELIDRRPLFPGR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 RMLTFNPLQRTITVEEALDHPYLRHLHDADEP 331
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 RMLTFNPLQRTITVTVRHEWHGGRFRPRTSHRDLFCHAVAEALAHPLYERLHDVDDDEP 360
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QY 332 ICLEPFESDFEQKALNEDQMKQLIFNEAIEKMPNIRY 368
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 VCTEFESDFEQKALNEDQMKQLIFNEAIEKMPNIRY 397
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-10-767-701-45777
; Sequence 45777, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45777
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C35159_1.pep
US-10-767-701-45777

Query Match      86.1%; Score 1682.5; DB 4; Length 374;
Best Local Similarity 87.3%; Pred. No. 1.6e-130;
Matches 322; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 MDGAPVAEPRPTVTHNGFLQYINIFGNLFEITHKYQPPIMPPIGRGAYGIVCSVMNFETRE 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 66 MVAIKKIANAFNDHMDAKRTLRREIKLLRLHLDHENIIGIRDVIPPPIPOAFNDVYIGTELW 125
 QY 121 DTDLHHIIRSNQELSEHCQFYQYILRLGLKYIHSANVTHRDLPKSNLLNANCDLKICD 180
 Db 126 DTDLHHIIRSNQELSEHCQFYQYILRLGLKYIHSANVSPDRSPSLLRSAMSFLLTSGV 185
 QY 181 FGLARPSSESDMMTEYVTVTRWRAPPELLNSTDYSA-DVWSVGCIFMELINRQPLPPGR 239
 Db 186 VAIKNTAYACDMMTEYVTVTRWRAPPELLNSTDYSAIDVWSVGCIFMELINRQPLPPGR 245
 QY 240 DHMHQRLITEVIGTPTDDELGRFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
 Db 246 DHMHQRLITEVIGTPTDDELGRFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 305
 QY 300 RMLTFNPLQRIITVEALDHPYLERLHDIADEPICLPPFSDFEQKALNEDQMKQLIFNEA 359
 Db 306 RMLTFNPLQRIITVEALDHPYLERLHDIADEPICLPPFSDFEQKALNEDQMKQLIFNEA 365
 QY 360 IENNPNIY 368
 Db 366 IENNPNIY 374

RESULT 5

US-10-732-923-1332
 ; Sequence 1332, Application US/10732923
 ; Publication No. US20050108791A1

; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 1332

; LENGTH: 376
 ; TYPE: PRT

; ORGANISM: Nicotiana benthamiana
 ; ORGANISM: Solanum tuberosum

US-10-732-923-1332

Query Match 75.6%; Score 1476.5; DB 5; Length 376;
 Best Local Similarity 72.7%; Pred. No. 1.6e-113;
 Matches 264; Conservative 57; Mismatches 41; Indels 1; Gaps 1;

QY 3 GAPVAFPRPTMTGGRYLLDYIFGNKFEVTKYQPPIMPITGRGAYGIVCSVMNFETREMV 62
 Db 11 GQGFPPPSVLTGGQYQYDIFGNFFETTKYRPPIMPITGRGAYGIVCSVMNFETREMV 70
 QY 63 AIKKIANAFNDMDAKRTLRREIKLLRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELMDT 122
 Db 71 AVKIANAFNDMDAKRTLRREIKLLRLHLDHENIIGIRDVIPPPIPPRRRFSVYIATELMDT 130
 QY 123 DLHHIIRSNQELSEHCQFYQYILRLGLKYIHSANVTHRDLPKSNLLNANCDLKICDFG 182
 Db 131 DLHHIIRSNQELSEHCQFYQYILRLGLKYIHSANVTHRDLPKSNLLNANCDLKICDFG 190
 QY 183 LARPSSESDMMTEYVTVTRWRAPPELLNSTDYSA-DVWSVGCIFMELINRQPLPPGRDH 241
 Db 191 LARPNTENEMTEYVTVTRWRAPPELLNSTDYTAIDVWSVGCIFMELINRQPLPPGRDH 250
 QY 242 MHQMLITEVIGTPTDDELGRFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERM 301
 Db 251 VHQRILTELLGTPTESDLSFLRNEDAKRYIRQLPQHPROQLANVFPVFNPLAIDLVDKM 310
 QY 302 LTFNPLQRIITVEALDHPYLERLHDIADEPICLPPFSDFEQKALNEDQMKQLIFNEAIE 361
 Db 311 LTLDPTRITVEALDHPYLERLHDIADEPICLPPFSDFEQKALNEDQMKQLIFNEAIE 370
 QY 362 MNP 364
 Db 371 LNP 373

RESULT 6

US-10-732-923-1324
 ; Sequence 1324, Application US/10732923
 ; Publication No. US20050108791A1

; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 1324

; LENGTH: 375
 ; TYPE: PRT

; ORGANISM: Capsicum annuum
 ; ORGANISM: Solanum tuberosum

US-10-732-923-1324

Query Match 74.8%; Score 1461.5; DB 5; Length 375;
 Best Local Similarity 72.7%; Pred. No. 2.8e-112;
 Matches 264; Conservative 52; Mismatches 46; Indels 1; Gaps 1;

QY 3 GAPVAFPRPTMTGGRYLLDYIFGNKFEVTKYQPPIMPITGRGAYGIVCSVMNFETREMV 62
 Db 10 GQGFPPPNIVTHGGQYQYDIFGNFFETTKYRPPIMPITGRGAYGIVCSVMNFETREMV 69
 QY 63 AIKKIANAFNDMDAKRTLRREIKLLRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELMDT 122
 Db 70 AVKIANAFNDMDAKRTLRREIKLLRLHLDHENIIGIRDVIPPPIPPRRRFSVYIATELMDT 129
 QY 123 DLHHIIRSNQELSEHCQFYQYILRLGLKYIHSANVTHRDLPKSNLLNANCDLKICDFG 182
 Db 130 DLHHIIRSNQELSEHCQFYQYILRLGLKYIHSANVTHRDLPKSNLLNANCDLKICDFG 189
 QY 183 LARPSSESDMMTEYVTVTRWRAPPELLNSTDYS-AADVWSVGCIFMELINRQPLPPGRDH 241
 Db 190 LARPNTENEMTEYVTVTRWRAPPELLNSTDYTAIDVWSVGCIFMELINRQPLPPGRDH 249
 QY 242 MHQMLITEVIGTPTDDELGRFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERM 301
 Db 250 VHQRILTELLGTPTESDLSFLRNEDAKRYIRQLPQHPROQLANVFPVFNPLAIDLVDKM 309
 QY 302 LTFNPLQRIITVEALDHPYLERLHDIADEPICLPPFSDFEQKALNEDQMKQLIFNEAIE 361
 Db 310 LTLNPTGRITVEALAHAPYLAKLHDAADPVPVPSDFEQQIGBEQIKDMYQEALV 369
 QY 362 MNP 364
 Db 370 LNP 372

RESULT 7

US-10-732-923-1446
 ; Sequence 1446, Application US/10732923
 ; Publication No. US20050108791A1

; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 1446

; LENGTH: 396
 ; TYPE: PRT

; ORGANISM: Solanum tuberosum
 ; ORGANISM: Solanum tuberosum

US-10-732-923-1446

Db 251 IQQLITELIGSPDDASLGFLRSDNAKRYMKQLPQFFRODFRLFRFNNMSPGAVDLLERM 310
Qy 302 LTFNPLQRI TVBEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQIFNEAIE 361
Db 311 LVFDPSSRI TVDEALHHPYLASLHDINEEPTCPAPFSFDFEQPSFTEAHIKELIWRESLA 370
Qy 362 MNPNIY 368
Db 371 FNPDPY 377

Search completed: December 27, 2005, 20:44:50
Job time : 166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:33:06 ; Search time 46 Seconds
(without alignments)

661.405 Million cell updates/sec

Title: US-10-768-886-2

Perfect score: 1953
Sequence: 1 MDGAPVAFRPTWTHGGRYL.....DQMKQLIFNEAIENPNIRY 368

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgm2_6/ptodata/1/iaa/6 COMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1504.5	77.0	371	1	US-08-837-593-6
2	1472.5	75.4	375	1	US-08-837-593-5
3	1472.5	75.4	375	2	US-08-837-593-2
4	1471.5	75.3	370	1	US-08-837-593-7
5	1448	74.1	387	1	US-08-837-593-4
6	1445.5	74.0	393	1	US-08-837-593-3
7	1438.5	73.7	393	1	US-08-837-593-2
8	1327.5	68.0	371	1	US-08-837-593-8
9	1260.5	64.5	375	2	US-08-837-593-34
10	1031	52.8	372	1	US-08-837-593-9
11	921.5	47.2	304	2	US-09-739-455-13
12	921.5	47.2	304	2	US-09-739-455-23
13	921.5	47.2	304	2	US-10-153-919-13
14	921.5	47.2	304	2	US-10-153-919-23
15	904	46.3	624	2	US-09-417-197-57
16	902	46.2	365	1	US-08-176-620A-2
17	902	46.2	365	1	US-08-463-862-2
18	902	46.2	365	1	US-08-461-985-2
19	902	46.2	365	1	US-08-458-887-2
20	902	46.2	365	2	US-08-932-787B-2
21	902	46.2	365	2	US-08-932-012C-2
22	902	46.2	365	2	US-08-888-818C-2
23	902	46.2	367	1	US-08-176-620A-11
24	902	46.2	367	1	US-08-461-985-11
25	896	45.9	353	1	US-08-176-620A-14
26	896	45.9	353	1	US-08-461-985-14
27	894	45.8	353	2	US-09-487-558B-116

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Sequence 14, Appli
Sequence 14, Appli
Sequence 1021, Ap
Sequence 25, Appli
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Sequence 39, Appli
Sequence 9, Appli
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Sequence 9919, Ap
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Sequence 1028, Ap
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Sequence 12, Appli
Sequence 4, Appli
Sequence 14, Appli

28 891 45.6 355 2 US-08-459-953A-8
29 891 45.6 355 2 US-09-393-212-8
30 891 45.6 379 2 US-09-411-628-14
31 891 45.6 379 2 US-10-174-794-14
32 891 45.6 379 2 US-09-538-092-1021
33 887 45.4 379 2 US-09-025-580-25
34 887 45.4 379 2 US-09-642-749-25
35 887 45.4 631 2 US-09-417-197-39
36 880 45.1 380 2 US-08-459-953A-9
37 880 45.1 380 2 US-09-393-212-9
38 879 45.0 379 2 US-08-622-277A-8
39 879 45.0 380 2 US-09-949-016-9919
40 878 45.0 360 2 US-09-457-040B-3
41 878 45.0 360 2 US-09-538-092-1028
42 877 44.9 358 1 US-08-176-620A-12
43 877 44.9 358 1 US-08-461-985-12
44 877 44.9 358 2 US-09-457-040B-4
45 877 44.9 360 2 US-08-622-277A-14

ALIGNMENTS

RESULT 1

US-08-837-593-6
; Sequence 6, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhucun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-6

QY 63 AIKKIANAFNDMDAKRTLEIKLRLHLDHENIIGIRVDVTPPIPOAFNDVYIATLMDT 122
Db 70 AVKKIANAFDIYNDAKRTLEIKLRLHLDHENIIGIRVDVTPPIPLRREFSDVYIATLMDT 129
QY 123 DLHIIIRSNQBLSEHCQYFLYQILRLGLKYIHSANVIHRDLKPSNLLNANCDLKICDFG 182
Db 130 DLHIIIRSNQBLSEHCQYFMYQLLRLGLKYIHSANVLRDLKPSNLLNANCDLKICDFG 189
QY 183 LARPSSEDMTTEYVTRWTRAPPELLNSTDYSAADVMSVGCIFMELINRQPLFGRDH 241
Db 190 LARPNIEENNTTEYVTRWTRAPPELLNSTDYSAADVMSVGCIFMELMNRKPLFGKDH 249
QY 242 MHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQALDIERM 301
Db 250 VHOIRLLTELLGPTTEADLGFQNEADAKYIRQLPQHPROQLAEVPHVPLAIDLVDKM 309
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADPEICLPFSFDFEQKALNEDQMQLIFNEAIE 361
Db 310 LTFDPTNRIITVEALDHPYLERLHDIADPEICLPFSFDFEQKALNEDQMQLIFNEAIE 369
QY 362 MNP 364
Db 370 LNP 372

RESULT 4

US-08-837-593-7
; Sequence 7, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

US-08-837-593-7

Query Match 75.3%; Score 1471.5; DB 1; Length 370;
Best Local Similarity 72.7%; Pred. No. 4e-145;
Matches 264; Conservative 58; Mismatches 40; Indels 1; Gaps 1;
QY 3 GAPVAEPRFTMTGGRYLLYDIFGNKPFVNTKYQRPIMPIGRGAYGIVCSVMNFETREMV 62
Db 5 GGOYTDFFPAVDTHGGQFISYDIFGSLFEITSKYRPPPIPIGRGAYGIVCSVLDTETNELV 64
QY 63 AIKKIANAFNDMDAKRTLEIKLRLHLDHENIIGIRVDVTPPIPOAFNDVYIATLMDT 122
Db 65 AMKKIANAFNDMDAKRTLEIKLRLHLDHENIIGIRVDVTPPIPOAFNDVYIATLMDT 124
QY 123 DLHIIIRSNQBLSEHCQYFLYQILRLGLKYIHSANVIHRDLKPSNLLNANCDLKICDFG 182
Db 125 DLHIIIRSNQBLSEHCQYFLYQILRLGLKYIHSANVIHRDLKPSNLLNANCDLKICDFG 184
QY 183 LARPSSEDMTTEYVTRWTRAPPELLNSTDYSAADVMSVGCIFMELINRQPLFGRDH 241
Db 185 LARPTSENDPMTTEYVTRWTRAPPELLNSTDYSAADVMSVGCIFMELMNRKPLFGKDH 244
QY 242 MHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQALDIERM 301
Db 245 VHOIRLLTELLGPTTESDGLFTNEDAKYIRQLPQHPROQLAEVPHVPLAIDLVDKM 304
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADPEICLPFSFDFEQKALNEDQMQLIFNEAIE 361
Db 305 LTFDPTNRIITVEALDHPYLERLHDIADPEICLPFSFDFEQKALNEDQMQLIFNEAIE 364
QY 362 MNP 364
Db 365 LNP 367

RESULT 5

US-08-837-593-4
; Sequence 4, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044


```

Db      310 AKRITVEDALNHPFLISLHNEBPVCDSPFNDFPEQASLSEDDIKELIWNELKPDPN 368
RESULT 9
US-09-828-313-34
; Sequence 34, Application US/09828313
; Patent No. 6867351
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-34

Query Match      64.5%; Score 1260.5; DB 2; Length 375;
Best Local Similarity 64.7%; Pred. No. 4.6e-123;
Matches 233; Conservative 55; Mismatches 71; Indels 1; Gaps 1;

QY      3 GAPVAFPRPTMTGGRYLLYDIFGNKFEVNTKYOPPIPIGRGAYGIVCSVMNFETREMV 62
Db      6 GPELVKVIPTVGGHVXKVAGTDFVTKPPLRPIGRGAYGIVCSLFDVTVTGEV 65
QY      63 AIKKNAFNNDMDAKRTLEIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATLMDT 122
Db      66 AVKKNAGFNDRIDAKRTLEIKLRLHLDHENVVAITDIIRPTRENFNDVVIYVELMDT 125
QY      123 DLHHTIRSNQELSEHCQYFLYQILRGLKYIHSANVHRLKPSNLLNANCDLKICDFG 182
Db      126 DLHQIIRSNQALTEHCQYFLYQILRGLKYIHSANVHRLDPTNLLVANCCLKIADFG 185
QY      183 LARPSSESDMTEYVYVTRWYRAPELLNSTDYSA-DVMSVGCIFMELINROPLPFGRDH 241
Db      186 LARTLSETDMTEYVYVTRWYRAPELLNCSAYTAAIDIVSGCIFMELNRSALPFGRDY 245
QY      242 HQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDLIERM 301
Db      246 VHQLRLITELIGTPEDRLGFLRSNDRARYIKHLPRQSPILPTQKPRGINRSALDIVERM 305
QY      302 LTFNPLQRTVEALDHPYLERLHDIADPEICLPPSPFPEQKALNEDQMKLI FNEAIE 361
Db      306 LVFDPKAKRITVEAALAHPLYLASLHDINDEPASVSPFEPDFEPPTSEEHIKOLINREALD 365

RESULT 10
US-08-837-593-9
; Sequence 9, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Kleesig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA

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; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-9

Query Match      52.8%; Score 1031; DB 1; Length 372;
Best Local Similarity 54.7%; Pred. No. 4.4e-99;
Matches 198; Conservative 68; Mismatches 90; Indels 6; Gaps 5;

QY      5 PVAFPRPTMTGGRYLLYDIFGNKFEVNTKYOPPIPIGRGAYGIVCSVMNFETREMVAI 64
Db      4 VPEPPNGRTPEKHV--YSMMQSLFEIDTKY-VPIKPIGRGAYGIVCSVNRETWEKVAI 60
QY      65 KKIANAFNNDMDAKRTLEIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATLMDTDL 124
Db      61 KKINAFENRIDALRTLEIKLRLHLDHENVIALKDVMPHRRSFKDVLYVYELMDTDL 120
QY      125 HHITRSNQLSEHCQYFLYQILRGLKYIHSANVHRLKPSNLLNANCDLKICDFGLA 184
Db      121 HQIIRSNQALTEHCQYFLYQILRGLKYIHSANILHRLDKPGLNLLINANCDLKICDFGLA 180
QY      185 RPSSSD-MMTYVYVTRWYRAPELLNSTDY-SAADVMSVGCIFMELINROPLPFGRDHM 242
Db      181 RTSGKQDFMTYVYVTRWYRAPELLNCCDNYGTSIDVMSVGCIFABLLGRKVPFPGTECL 240
QY      243 HQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDLIERM 302
Db      241 NQLKLIINILGQREEDIEFDINPKARKYIKSLPSPCTPFSRLYPHAHLAIDLQRL 300
QY      303 TFPNPLQRTVEALDHPYLERLHDIADPEICLPPSPFPEQKALNEDQMKLI FNEAIE 362
Db      301 VFDPSKRISVIEALQHPYMSPLYDNTDPPAQVPINLIDED-LGEETIREMMWSEILEY 359
QY      363 NP 364
Db      360 HP 361

RESULT 11
US-09-739-455-13
; Sequence 13, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:

```


; PRIOR APPLICATION NUMBER: 60/209,585
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/739,455
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Dictyostelium discoideum
US-10-153-919-23

Query Match 47.2%; Score 921.5; DB 2; Length 304;
Best Local Similarity 59.2%; Pred. No. 9.1e-88;
Matches 174; Conservative 52; Mismatches 63; Indels 5; Gaps 3;

QY 42 IGRGAYGVCSVMNFTREVMVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDV 101
DB 11 IGHGAYGVVCSAKDNLTGSEKVAIKKISKAFDNLKDTKRTLRKILRLHLDHFKHENLISIKDI 70
QY 102 IPPPIPOAFNDVYIATLMDTDLHHIIRSNQELSEHCOVFLYOILRGLKYIHSANVHR 161
DB 71 LKNSKEQEDVYIVSELMDTDLHQIITSQPPLSDHCHQFYVQMLRGLKHIHSANVLR 130
QY 162 DLKPSNLLNANCDLKICDPGLAR--PSSSDMMTEYVVRWYRAPELLLNSTDYS--AAD 218
DB 131 DLKPSNLLINEDCLLKICDGLARVEDATHQGFMTYVATRWYRAPEVILSWNKYTKAID 190
QY 219 VNSVGCIFMELINRQPLFGDRHMQRLITEVIGTPTDDELGFIBNEDARKYMR--HLP 276
DB 191 INSVGCIFAEILGRKPLFOGKYIHOITLIETIGSPSEEDICNIANEQARQPIRSLNMG 250
QY 277 QYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTVVEALDHPYLRRLHLDIADE 330
DB 251 NQPKVFNANFPKPNDAIDLLERMLYFDPSEKLTVEEALAHYPQSLHDPDSDE 304

RESULT 15
US-09-417-197-57
; Sequence 57, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mERK1-F64L-S65T-GFP fusion
US-09-417-197-57

Query Match 46.3%; Score 904; DB 2; Length 624;
Best Local Similarity 50.9%; Pred. No. 1.8e-85;
Matches 175; Conservative 65; Mismatches 96; Indels 8; Gaps 5;
QY 26 GNKFEVTNKQPPIMPTIGRGAYGVCSVMNFTREVMVAIKKIANAFNNDMDAKRTLRLEIK 85
DB 34 GQPFVGVGRY-TQLQYIGEGAYGNVSSAYDVRKTRVAIKKI-SPFEHQYTCQRTLRLEIQ 91
QY 86 LLRLHLDHENIIGIRDVTPPIPOAFNDVYIATLMDTDLHHIIRSNQELSEHCOVFLYQ 145
DB 92 ILLRFRHENVIGIRDILRAPTRLEAMRDVYIVQDLMETDLYKLKLS-QQLSNDHICYFLYQ 150
QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDGLAR----PSSSDMMTEYVVRW 201
DB 151 ILRGLKYIHSANVLRDLKPSNLLINTTCDLKI CDGLARIADPEHDHGTGLTEYVATRW 210

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OM protein - protein search, using sw model
Run on: December 27, 2005, 20:30:11 ; Search time 39 Seconds
(without alignments)
907.892 Million cell updates/sec

Title: US-10-768-886-2
Perfect score: 1953
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DQKQLIFNEAIEMPNIRY 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819.5	93.2	369	2 S56638	mitogen-activated
2	1504.5	77.0	371	2 T09622	protein kinase MMK
3	1472.5	75.4	370	2 T47504	mitogen-activated
4	1472.5	75.4	375	2 T03971	mitogen-activated
5	1471.5	75.3	370	2 S40469	mitogen-activated
6	1448	74.1	387	2 S48123	mitogen-activated
7	1445.5	74.0	393	2 S51321	mitogen-activated
8	1442	73.8	395	2 S40472	mitogen-activated
9	1441.5	73.8	371	2 T14915	mitogen-activated
10	1437	73.6	394	2 S33635	mitogen-activated
11	1327.5	68.0	371	2 S51320	mitogen-activated
12	1325.5	67.9	371	2 S60121	mitogen-activated
13	1315.5	67.4	376	2 S40470	mitogen-activated
14	1277.5	65.4	369	2 C86146	hypothetical prote
15	1257.5	64.4	376	2 S40471	mitogen-activated
16	1244.5	63.7	363	2 C86214	hypothetical prote
17	1230	63.0	373	2 T13024	probable protein k
18	1229	62.9	393	2 T47803	mitogen-activated
19	1210.5	62.0	406	2 D84898	probable mitogen-a
20	1031	52.8	372	2 S39559	mitogen-activated
21	1024	52.4	415	2 A56042	mitogen-activated
22	1017	52.1	384	2 S52989	mitogen-activated,
23	981	50.2	370	2 F86236	protein F14N23.9 [
24	979	50.1	368	2 B84561	MAP kinase (ATMPK7
25	972	49.8	368	2 S40473	mitogen-activated
26	966	49.5	376	2 F96619	protein T30B16.13
27	940	48.1	361	2 C85430	MAP kinase like pr
28	923.5	47.3	356	2 T51944	pathogenicity MAP
29	906	46.4	361	2 T51943	mitogen-activated

30	904	46.3	377	2 S28184	Ca2+/calmodulin-de
31	902	46.2	380	2 JC1451	Ca2+/calmodulin-de
32	902	46.2	392	2 JW0052	extracellular sign
33	901	46.1	369	2 A60041	Ca2+/calmodulin-de
34	898	46.0	376	2 A36978	MAP kinase mpk-1 (
35	898	46.0	444	2 A36977	MAP kinase sur-1 (
36	897	45.9	372	2 S15663	protein kinase (EC
37	894	45.8	353	2 S28548	protein kinase (EC
38	887	45.4	379	1 A48082	MAP kinase 3 (EC 2
39	878	45.0	360	1 JQ1400	MAP kinase 1 (EC 2
40	877	44.9	358	2 S16444	mitogen-activated
41	877	44.9	358	2 A40033	protein kinase (EC
42	877	44.9	360	2 S25011	protein kinase (EC
43	877	44.9	369	2 JW0053	extracellular sign
44	862	44.1	361	2 A39754	mitogen-activated
45	855.5	43.8	362	2 A47211	protein kinase ERK

ALIGNMENTS

RESULT 1

S56638
mitogen-activated protein kinase 1 homolog (clone AspK9) - oat
N;Alternate names: MAP1 kinase
C;Species: Avena sativa (oat)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56638
R;Huttly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A;Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that sho
A;Reference number: S56638; MUID:95284341; PMID:7766874
A;Accession: S56638
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-369 <HUT>
A;Cross-references: UNIPROT:Q43379; UNIPARC:UPI00000AA427; EMBL:X79993; NID:9871983; PI
C;Superfamily: Kinase-related transforming protein; protein kinase
C;Keywords: ATP; phosphotransferase; protein kinase
F;33-322/Domain: protein kinase homology <KIN>
F;42-50/Region: protein kinase ATP-binding motif

Query Match	93.2%;	Score	1819.5;	DB 2;	Length	369;			
Best Local Similarity	91.3%;	Pred. No.	7.3e-69;						
Matches	337;	Conservative	20;	Mismatches	11;	Indels	1;	Gaps	1;
Qy	1	MDGAPVAEPRPTWTHGGRYLLYDIFGNKPEVTWKYQPPIMPICRGAYGIVCSVMNPFTR	60						
Db	1	MDGAPVAEPRPTWTHGGRFLYLYINFGNQFEITSKYQPPIMPICRGAYGIVCSVMNPFTR	60						
Qy	61	MVAIKKIANAFNNDMDAKRTLREIKLLRHLHDHENIIGIRDVIPPPIQAFNDVVIATELM	120						
Db	61	MVAIKKIANAFNNDMDAKRTLREIKLLRHLHDHENIVGLRDVIPPSPISQSFNDVVIATELM	120						
Qy	121	DTDLHHIIRSNQSLSEHCQFLYQLRGKLYTHSANVHRDLKPSNLLNANCDLKICD	180						
Db	121	DTDLHHIIRSNQSLSEHCQFLYQLLRGKLYTHSANVHRDLKPSNLLNANCDLKICD	180						
Qy	181	FGLARPSSSDMMTEVVTWYRAPPELLNSTDYSAA-DVWSVGCIFMELINRQPLPFR	239						
Db	181	FGLARPSSSDMMTEVVTWYRAPPELLNSTDYSAAIDVWSVGCIFMELINRAPLPFR	240						
Qy	240	DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLQYPRRTFASMPFVQPAALDLIE	299						
Db	241	DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLQYPRRPFGQPKVQPAALDLIE	300						
Qy	300	RMLTFNPLQRIITVEEALDHPYLERLHDIADEPTCLEPFPDFEQKALNEQMKQLIFNEA	359						
Db	301	RMLTFNPLQRIITVEEALDHPYLERLHDVADEPTCTDFPSDFEQHPTEQMKQLIFNEA	360						
Qy	360	IENPNIRY 368							
Db	361	LELNPFRY 369							

```
RESULT 2
T09622
protein kinase MMK4 (EC 2.7.1.-), cold- and drought-induced - alfalfa
C:Species: Medicago sativa (alfalfa)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09622
R:Jonak, C.; Kiegerl, S.; Lighter, W.; Barker, P.; Huskisson, N.; Hirt, H.
Proc. Natl. Acad. Sci. U.S.A. 93, 11274-11279, 1996
A:Title: Signaling in plants: a mitogen-activated protein kinase pathway is activated by
A:Reference number: Z16782; MUID:97008170; PMID:8855346
A:Accession: T09622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-371 <JON>
A:Cross-references: UNIPROT:Q24077; UNIPARC:UPI00000A8D84; EMBL:X82270; NID:g1667372; PI
C:Genetic:
A:Gene: MMK4
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase; protein kinase
F:36-325/Domain: protein kinase homology <KIN>

Query Match 77.0%; Score 1504.5; DB 2; Length 371;
Best Local Similarity 74.4%; Pred. No. 7e-56;
Matches 268; Conservative 56; Mismatches 35; Indels 1; Gaps 1;

QY 6 VAEFRPTMTGGRYLLYDIFGNKFEVTNKKYQPPIMPIGRGAYGIVCSVMNFETREMVATK 65
DB 9 VAEFPVAVQTHGGQFQYVNGNDVFVTAKYRPPIMPIGRGAYGIVCSLNTETNELVAVK 68
QY 66 KIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELMDTLH 125
DB 69 KIANAFDNHMDAKRTLREIKLRLHLDHENVIGLRDVPPLRREFNDVVIATELMDTLH 128
QY 126 HIIRSNQELSEHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKICDPGLAR 185
DB 129 QIIRSNQELSDHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKIIDFGLAR 188
QY 186 PSSESMDMTEYVVTWRYRAPELLNSTDY-SAADVMSVGCIFMELINRQPLPFGRDHMQ 244
DB 189 PTMESDFMTEYVVTWRYRAPELLNSTDYSAIDVMSVGCIFMELNNKPKLPFGKDKHMQ 248
QY 245 MRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYRRTFASMPFRVQPAALDLIERMLTF 304
DB 249 MRLITELLGPTDADVLKNDADRYIRQLPOYRQPLNRVFPVHPLAIDLVDKMLTI 308
QY 305 NPLQRTVTEALDHPYLERLHDIADPEPICLEPSPDFEQKALNEDQMOLIFNEAIEEMP 364
DB 309 DPTRITVTEALAHPLYLEKLDVADBPICWEPSPDFEQQLHDEQIKEMIYREALALNP 368

RESULT 3
T47504
mitogen-activated protein kinase 3 - Arabidopsis thaliana
N:Alternate names: protein F9K21.220
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47504
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24467
A:Accession: T47504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <JON>
A:Cross-references: UNIPROT:Q39023; UNIPARC:UPI0000001AE1; EMBL:AL138657
A:Experimental source: cultivar Columbia; BAC clone F9K21
C:Genetic:
A:Map position: 3
A:Introns: 53/2; 96/3; 142/3; 253/3; 315/1
A>Note: F9K21.220
C:Superfamily: Kinase-related transforming protein; protein kinase homology
```

```
Query Match 75.4%; Score 1472.5; DB 2; Length 370;
Best Local Similarity 72.7%; Pred. No. 1.5e-54;
Matches 264; Conservative 58; Mismatches 40; Indels 1; Gaps 1;

QY 3 GAPVAEFPRTMTGGRYLLYDIFGNKFEVTNKKYQPPIMPIGRGAYGIVCSVMNFETREMV 62
DB 5 GGOYTFDPAVETHGGQFISYDIFGSLFETTKYRPPIMPIGRGAYGIVCSVLDTETNELV 64
QY 63 AIKKTANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELMDT 122
DB 65 AMKKTANAFDNHMDAKRTLREIKLRLHLDHENIIRDVVPPPLRREFSDVVIATELMDT 124
QY 123 DLHIIIRSNQELSEHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 125 DLHIIIRSNQSLSEHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKICDPG 184
QY 183 LARPSSESMDMTEYVVTWRYRAPELLNSTDYSA-DVMSVGCIFMELINRQPLPFGRDH 241
DB 185 LARPTSENDPMTEYVVTWRYRAPELLNSTDYTAIDVMSVGCIFMELNNKPKLPFGKDH 244
QY 242 MHQWELITEVIGTPTDDELGFIRNEDARKYMRHLPOYRRTFASMPFRVQPAALDLIERM 301
DB 245 VHQMELLTELLGPTDESOLGFTNEDAKRYIRQLPNFPQPLAKULFSHVNPMAIDLVDKM 304
QY 302 LTFNPLQRTVTEALDHPYLERLHDIADPEPICLEPSPDFEQKALNEDQMOLIFNEAIE 361
DB 305 LTFDPNRRITVEQALNHQYLAKLHDPNDEPICQKPFSEFEQOPLDEQIKEMIYQEAIA 364
QY 362 MNP 364
DB 365 LNP 367

RESULT 4
T03971
mitogen-activated protein kinase (EC 2.7.1.-) WIPK - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03971
R:Seo, S.; Okamoto, M.; Seto, H.; Ishizuka, K.; Sano, H.; Ohashi, Y.
Science 270, 1988-1992, 1995
A:Title: Tobacco MAP kinase: a possible mediator in wound signal transduction pathways.
A:Reference number: Z15170; MUID:96123271; PMID:8533090
A:Accession: T03971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-375 <SEO>
A:Cross-references: UNIPROT:Q40598; UNIPARC:UPI00000A4PF8; EMBL:D61377; NID:g1136297; P;
C:Comment: MAP kinase is part of the initial response of higher plants to mechanical wou
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:40-329/Domain: protein kinase homology <KIN>

Query Match 75.4%; Score 1472.5; DB 2; Length 375;
Best Local Similarity 72.5%; Pred. No. 1.5e-54;
Matches 263; Conservative 58; Mismatches 41; Indels 1; Gaps 1;

QY 3 GAPVAEFPRTMTGGRYLLYDIFGNKFEVTNKKYQPPIMPIGRGAYGIVCSVMNFETREMV 62
DB 10 GGOFPDPFSPVLTHGGQYVQDFIDGFFETTKYRPPIMPIGRGAYGIVCSVLNTSLNEMV 69
QY 63 AIKKTANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELMDT 122
DB 70 AVKKTANAFDYMNDAKRTLREIKLRLHLDHENVIGLRDVPPLRREFSDVVIATELMDT 129
QY 123 DLHIIIRSNQELSEHCQFLYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 130 DLHIIIRSNQGLSEDHCQFYFVQLRGLKYIHSANVLHRLKPSNLLNANCDLKICDPG 189
QY 183 LARPSSESMDMTEYVVTWRYRAPELLNSTDYSA-DVMSVGCIFMELINRQPLPFGRDH 241
DB 190 LARPNIENNTTEYVVTWRYRAPELLNSTDYTAIDVMSVGCIFMELNNKPKLPFGKDH 249
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A;Cross-references: UNIPROT:Q40532; UNIPARC:UPI0000130582; EMBL:X63880; NID:G634069; PID: C;Genetics:

A;Gene: ntif4

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

P;57-345/Domain: protein kinase homology <KIN>

P;56-74/Region: protein kinase ATP-binding motif

Query Match 74.0%; Score 1445.5; DB 2; Length 393;
Best Local Similarity 72.6%; Pred. No. 2e-53;
Matches 267; Conservative 52; Mismatches 44; Indels 5; Gaps 3;

QY 5 PVA---EPRTWTHGGRYLLYDIFGNKFEVTKYQPPIMPGRGAYGVCSVWVFTRM 61
DB 26 PVAGIDNIPATLSHGGRFIQYINFGNIFEVTKYKPPIMPGRGAYGVCSALNSNTH 85
QY 62 VALKIANAFNDMDAKRTLRKLRHLDHENIIGIRDVIPPPIPOAFNDVYATLMD 121
DB 86 VALKIANAFNDKIDAKRTLRKLRHLDHENIVAIRDIIPPPQREAFNDVYATLMD 145
QY 122 TDLHIIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 181
DB 146 TDLHQIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 205
QY 182 GLARPSSEDMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELINQPLPPGRD 240
DB 206 GLARVTSDFMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELMDRKPLPPGRD 265
QY 241 HHOMELITEVIGTPTDDELGPTNRDARKYHMLPOYPRRTFASMPRVPQALDLIER 300
DB 266 HHQLRLMELIGTPTSEAEFV-NENAKYIRQLPPYRQRFVFPVHPVPAIDLVEK 324
QY 301 MLTFNPLQRTVBEALDHPYLERLHDADEPICLEPFSDFEQKALNEDQMQLIFNEAI 360
DB 325 MLTFDPRRTITVEDALAHPLTSLHDSDEPVCMTFFNDFEQHALTEQMKELIYREGI 384
QY 361 ENMPNTRY 368
DB 385 AFNPEYQH 392

RESULT 8

S40472

mitogen-activated protein kinase 6 (EC 2.7.1.1) - Arabidopsis thaliana

N;Alternate names: MAP kinase (ATMPK6)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 06-Oct-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004

C;Accession: S40472; E84870

R;Wizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kanada, H.; Shinozaki, K. FEBS Lett. 336, 440-444, 1993

A;Title: ATMPK6: a gene family of plant MAP kinases in Arabidopsis thaliana.

A;Reference number: S40469; MUID:94109583; PMID:8282107

A;Accession: S40472

A;Molecule type: mRNA

A;Residues: 1-395 <MIZ>

A;Cross-references: UNIPROT:Q39026; UNIPARC:UPI000000148F; EMBL:D21842; NID:G457403; PID: R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84870

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <STO>

A;Cross-references: UNIPARC:UPI000000148F; GB:AE002093; NID:G2281091; PIDN:AAB64027.1; C;Genetics:

A;Gene: MPK6; At2g43790

A;Map position: 2

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

P;60-348/Domain: protein kinase homology <KIN>

F;69-77/Region: protein kinase ATP-binding motif

Query Match 73.8%; Score 1442; DB 2; Length 395;
Best Local Similarity 72.4%; Pred. No. 2.8e-53;
Matches 270; Conservative 46; Mismatches 45; Indels 12; Gaps 3;

QY 3 GAPVAEFRP-----TWTHGGRYLLYDIFGNKFEVTKYQPPIMPGRGAYGVCS 52
DB 20 GPPAAAPSPQMPGIENIPATLSHGGRFIQYINFGNIFEVTKYKPPIMPGRGAYGVCS 79
QY 53 VVNPETREWVAIKKIANAFNDMDAKRTLRKLRHLDHENIIGIRDVIPPPIPOAFND 112
DB 80 ANNSTNSVAIKKIANAFNDKIDAKRTLRKLRHLDHENIVAIRDIIPPPLRNAFND 139
QY 113 VYIATLMDTDLHIIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNA 172
DB 140 VYIATLMDTDLHIIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNA 199
QY 173 NCDLKICDFGLARPSSEDMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELIN 231
DB 200 NCDLKICDFGLARVTSDFMTEYVVTWYRAPELLLNSTDYSAAIDVMSVGCIFMELMD 259
QY 232 RQPLPGRDHMHOMELITEVIGTPTDDELGPTNRDARKYHMLPOYPRRTFASMPRVPQ 291
DB 260 RKPLPGRDHVHQLRLMELIGTPTSEAEFV-NENAKYIRQLPPYRQRFVFPVHPV 318
QY 292 PAALDLIERMTFNPLQRTVBEALDHPYLERLHDADEPICLEPFSDFEQKALNEDQM 351
DB 319 FLAIDLEKMLTDFDPRRTITVEDALAHPLTSLHDSDEPCTIPFDFENHALSEEQM 378
QY 352 KQLIFNEAIENMP 364
DB 379 KELIYREALAFNP 391

RESULT 9

T14915

mitogen-activated protein kinase I (EC 2.7.1.1) - parsley

N;Alternate names: MAP kinase I

C;Species: Petroselinum crispum (parsley)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14915

R;Jugierink, W.; Kroj, T.; zur Nieden, U.; Hirt, H.; Scheel, D. Science 276, 2054-2057, 1997

A;Title: Receptor-mediated activation of a MAP kinase in pathogen defense of plants.

A;Reference number: Z18265; MUID:97342856; PMID:9197271

A;Accession: T14915

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-371 <LIIG>

A;Cross-references: UNIPROT:O04694; UNIPARC:UPI00000A9255; EMBL:Y12785; NID:G2231033; PID: C;Comment: MAP kinase is part of the initial response of higher plants to mechanical wounding

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase

F;36-325/Domain: protein kinase homology <KIN>

Query Match 73.8%; Score 1441.5; DB 2; Length 371;
Best Local Similarity 72.1%; Pred. No. 2.8e-53;
Matches 259; Conservative 56; Mismatches 43; Indels 1; Gaps 1;

QY 8 EPRPTWTHGGRYLLYDIFGNKFEVTKYQPPIMPGRGAYGVCSVWVFTRMVAIKKI 67
DB 11 DFPATQTHGGRFIQYINFGNIFQVTKYRPPIMPGRGAYGVCSIMNTETNMVAVKKI 70
QY 68 ANAFNDMDAKRTLRKLRHLDHENIIGIRDVIPPPIPOAFNDVYATLMDTDLHII 127
DB 71 ANAFNDMDAKRTLRKLRHLDHENIVAIRDIIPPPLRREFTDVYIATLMDTDLHQI 130
QY 128 IRSNQLSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS 187
DB 131 IRSNQLSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARHN 190
QY 188 SESDMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELINQPLPPGRDHMHQMR 246

[illegible][illegible]


```
||||:||||| ||| ||: ||: ||: || ||||| :| ||: ||: ||: ||: ||: ||: ||
Db 314 RITVDEALCHPYLAPLHEYNEEPCVRPFHDFEQPSLSTEENIKELIYRESVKFNP 369

RESULT 15
S40471
mitogen-activated protein kinase 5 (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Sep-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: S40471
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 336, 440-444, 1993
A;Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.
A;Reference number: S40469; MUID:94109583; PMID:8282107
A;Accession: S40471
A;Molecule type: mRNA
A;Residues: 1-376 <MIZ>
A;Cross-references: UNIPROT:Q39025; UNIPARC:UPI000016DA9E; EMBL:D21841; NID:9457401; PIR:
C;Genetics:
A;Gene: MPK5
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;40-298/Domain: protein kinase homology <KIN>
F;49-57/Region: protein kinase ATP-binding motif

Query Match 64.4%; Score 1257.5; DB 2; Length 376;
Best Local Similarity 63.7%; Pred. No. 1.1e-45;
Matches 225; Conservative 66; Mismatches 61; Indels 1; Gaps 1;

QY 13 MTHGGRYLLYDIQGNKEFTVNTKYQPPIMPITGRGAYGIVCSVMNFTETREMYAIKKIANAFN 72
Db 20 LVHGGRYFYQNVYGNDFEVSNNKYVPPIRPIRGAYGVCVADVSETHETAIKKIGKAFD 79
QY 73 NDMDAKRTLRKIKLRHLDHENIIGIRDVIPPPIPOAFNDVYIATELMDTDLHHIIRSNQ 132
Db 80 NKVDAKRTLRKIKLRHLEHENVVIXDIIRPKKEDFDVYIVFELMDTDLHQIIRSNQ 139
QY 133 ELSEHCQYPLYQILRGLKTYHSANVIRDLKPSNLLNANCDLKICDFGLARPSSESDM 192
Db 140 SLNDDHCQYPLYQILRGLKTYHSANVIRDLKPSNLLNANCDLKITDFGLARTTSETY 199
QY 193 MTEYVTVTRWYRAPELLNSTDY-SAADVMSVGCIFMELINRQPLFGRDHMQRLITEV 251
Db 200 MTEYVTVTRWYRAPELLNSSEYTSADVMSVGCIFAFIMTREPFPFGKQYVHQKLITEL 259
QY 252 IGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRI 311
Db 260 IGSFDGNSLEFLSANGGKVKELPKFPQNFSARPPSMNSTAIDLLEKMLVDFPVKRI 319
QY 312 VREALDHPYLERLHDIADEPICLEPFSDFEQKALNEDOMKQIFNEAIEMNP 364
Db 320 VREALCPYLSALHDLNDEPVCSNHFSDPFSDPSTEEIKELVWLESVKFNP 372

Search completed: December 27, 2005, 20:41:08
Job time : 41 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:20:31 ; Search time 188 Seconds
(without alignments)
860.061 Million cell updates/sec

Title: US-10-768-886-2
Perfect score: 1953
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DOMKQLIFNEALEMPNIRY 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 15 summaries

Database : A Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	368	8	ADT02330 Rice mito
2	1803.5	92.3	374	3	AAG34157 Zea mays
3	1798.5	92.1	374	4	AAB48046 Signal tr
4	1632.5	83.6	330	3	AAG34158 Zea mays
5	1557.5	79.7	316	3	AAG34159 Zea mays
6	1472.5	75.4	375	2	AAW15512 MAP kinas
7	1448.5	74.2	398	4	AAB48048 Signal tr
8	1442	73.8	382	3	AAG31654 Arabidops
9	1442	73.8	395	3	AAG31653 Arabidops
10	1441	73.8	366	3	AAG31655 Arabidops
11	1438.5	73.7	393	2	AAW61252 Salicylic
12	1423	72.9	398	4	AAB48047 Signal tr
13	1380.5	70.7	423	2	AAW15513 MAP kinas
14	1340.5	68.6	318	8	ADXT7953 Plant ful
15	1334.5	68.3	266	8	ADT02332 Rice mito
16	1331.5	68.2	403	8	ADY11673 Plant ful
17	1325.5	67.9	372	3	AAG33123 Zea mays
18	1325.5	67.9	372	4	AAB48044 Signal tr
19	1325.5	67.9	380	8	ADY11385 Plant ful
20	1320.5	67.6	358	3	AAG33124 Zea mays
21	1316.5	67.4	376	3	AAG04672 Arabidops
22	1279	65.5	371	3	AAG45420 Arabidops
23	1232.5	63.1	373	8	ADT60480 Plant pol
24	1230	63.0	373	3	AAG30672 Arabidops

25	1210.5	62.0	372	3	AAG42613 Arabidops
26	1210.5	62.0	406	3	AAG42612 Arabidops
27	1208.5	61.9	372	3	AAG06702 Arabidops
28	1208.5	61.9	379	3	AAG06701 Arabidops
29	1173.5	60.1	354	3	AAG30978 Arabidops
30	1103.5	56.5	311	5	AAM52837 Physcomit
31	1074.5	55.0	216	8	ADX73133 Plant ful
32	1031.5	52.8	280	3	AAG04673 Arabidops
33	1020.5	52.3	280	3	AAG33125 Zea mays
34	1015	52.0	366	3	AAG44681 Zea mays
35	1015	52.0	367	3	AAG44680 Zea mays
36	1015	52.0	369	3	AAG44679 Zea mays
37	1015	52.0	369	7	ABM74137 DNA clone
38	1014	51.9	369	4	AAB48043 Signal tr
39	1003.5	51.4	370	8	ADT60889 Plant pol
40	1003	51.4	367	3	AAG44793 Zea mays
41	1003	51.4	368	3	AAG44792 Zea mays
42	1003	51.4	368	3	AAG35746 Zea mays
43	1003	51.4	370	3	AAG44791 Zea mays
44	1003	51.4	370	3	AAG35745 Zea mays
45	1003	51.4	370	4	AAB48045 Signal tr

ALIGNMENTS

RESULT 1
ADT02330
ID ADT02330 standard; protein; 368 AA.
XX
AC ADT02330;
XX
-DT 13-JAN-2005 (first entry)
XX
DE Rice mitogen-activated protein kinase 5a (MAPK5a) polypeptide.
XX
KW Rice; mitogen-activated protein kinase 5a; MAPK5; MAPK5a;
KW abiotic stress tolerance; biotic stress tolerance; drought; temperature;
KW salinity; plant; enzyme.
XX
OS Oryza sativa.
XX
PH Key Location/Qualifiers
FT Misc-difference 218 /note= "Encoded by ATGCAC"
FT
XX
PN US2004209325-A1.
XX
PD 21-OCT-2004.
XX
PF 31-JAN-2004; 2004US-00768886.
XX
PR 31-JAN-2003; 2003US-0444249P.
XX
PA (YANG/) YANG Y.
XX
PA (XIONG/) XIONG L.
XX
YANG Y, Xiong L;
WPI; 2004-747214/73.
N-PSDB; ADT023329.
PT New isolated nucleic acid molecule encoding a mitogen-activated protein
PT kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic
PT and biotic stress in plants.
PS Claim 24; SEQ ID NO 2; 36pp; English.
XX
CC The invention relates to a rice mitogen-activated protein kinase 5
CC (MAPK5) polypeptides and the polynucleotides encoding them. The invention
CC also relates to an antibody that specifically binds to a peptide
CC consisting of a C-terminal portion of a MAPK5 polypeptide, a transgenic
CC plant transformed by a polynucleotide encoding a MAPK5 orthologue where

CC over expression of the MAPK5 orthologue in the plant results in increased
 CC tolerance to abiotic stress compared to a wild-type plant and a method
 CC for evaluating a plant for tolerance to abiotic stress comprising
 CC treating a plant with abiotic stress, isolating a MAPK5 protein from the
 CC plant, detecting MAPK5 activity and evaluating the increase or decrease
 CC in MAPK5 activity in the plant where the increase in MAPK5 activity
 CC indicates the plant is tolerant to abiotic stress. The methods and
 CC compositions of the present invention are useful for increasing tolerance
 CC to abiotic and biotic stress in plants using MAPK5, where the abiotic
 CC stress is drought, temperature or salinity and the biotic stress is from
 CC pathogenic bacteria, viruses, nematodes and insects. This sequence
 CC represents the rice MAPK5a polypeptide of the invention.

XX Sequence 368 AA;

Query Match 100.0%; Score 1953; DB 8; Length 368;

Best Local Similarity 100.0%; Pred. No. 8.5e-192;

Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGAPVAEPRPTWTHGGRVLLYDFGNKFEVTKYQPPIMPIGRGAYGIVCSVMNPETRE 60

DB 1 MDGAPVAEPRPTWTHGGRVLLYDFGNKFEVTKYQPPIMPIGRGAYGIVCSVMNPETRE 60

QY 61 MVAIKKIANAFNNDMDAKRTLEIKLRLHLDHENIIGIRDVIPPPIQAPFNDVVIATELM 120

DB 61 MVAIKKIANAFNNDMDAKRTLEIKLRLHLDHENIIGIRDVIPPPIQAPFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFYQLRGLKYIHSANVTHRDLPKSNLLLNANCDLKICD 180

DB 121 DTDLHHIIRSNQELSEHCQFYQLRGLKYIHSANVTHRDLPKSNLLLNANCDLKICD 180

QY 181 FGLARPSSSDMTVEVYTWYRAPPELLNSTDYSAADVWSVGCIFMELINRQPLPFGRD 240

DB 181 FGLARPSSSDMTVEVYTWYRAPPELLNSTDYSAADVWSVGCIFMELINRQPLPFGRD 240

QY 241 HHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIER 300

DB 241 HHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIER 300

QY 301 MLTFNPLQRTVBEALDHPYLERLHDIADEPICLEPFSDFEQKALNEDQKQLIFNEAI 360

DB 301 MLTFNPLQRTVBEALDHPYLERLHDIADEPICLEPFSDFEQKALNEDQKQLIFNEAI 360

QY 361 ENMPNIRY 368

DB 361 ENMPNIRY 368

RESULT 2

AAG34157

ID AAG34157 standard; protein; 374 AA.

XX AAG34157;

AC AAG34157;

XX 18-OCT-2000 (first entry)

DT Zea mays protein fragment SEQ ID NO: 41518.

DE Zea mays subsp. mays.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence; corn.

XX Zea mays subsp. mays.

OS Zea mays subsp. mays.

XX EP1033405-A2.

PN 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

FR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130049P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

DE	Signal transduction protein.	
XX	Zea mays; maize; signal transduction protein; phytohormone; ethylene;	
KW	auxin; cytokinin; gibberellin; immunogen.	
XX		
OS	Zea mays.	
XX	WO20070059-A2.	
XX	23-NOV-2000.	
XX	28-APR-2000; 2000WO-US011687.	
XX	14-MAY-1999; 99US-0134292P.	
XX	08-JUL-1999; 99US-0142996P.	
XX	(PION-) PIONEER HI-BRED INT INC.	
PA	Helentjaris TG;	
XX		
XX	WPI; 2001-031929/04.	
DR	N-PSDB; AAC64259.	
XX		
PT	New signal transduction nucleic acids and encoded proteins useful for	
PT	regulating phytohormone expression, including ethylene, auxins,	
PT	cytokinins and gibberellin, to provide control of plant response to	
PT	environmental stresses.	
XX		
PS	Claim 13; Page 91; 136pp; English.	
XX		
CC	The invention provides Zea mays signal transduction proteins and encoding	
CC	nucleotide sequences. The nucleic acids are useful for regulating	
CC	expression of phytohormones, including ethylene, auxins, cytokinins, and	
CC	gibberellin, to effect developmental changes in plants and provide	
CC	control of plant response to environmental stresses. They may also be	
CC	used as probes or amplification primers in the detection, quantitation or	
CC	isolation of gene transcripts, for detecting mutations in the gene, for	
CC	monitoring upregulation of expression or changes in enzyme activity in	
CC	screening assays of compounds, for detection of any number of allelic	
CC	variants, or for site-directed mutagenesis in eukaryotic cells. They may	
CC	further be used for recombinant expression of their encoded polypeptides,	
CC	as immunogens in the preparation or screening of antibodies, and in sense	
CC	or antisense suppression of genes in a host cell, tissue or plant. The	
CC	proteins may be used in assays for enzyme agonists or antagonists, as	
CC	immunogens or antigens to obtain antibodies specifically immunoreactive	
CC	with the proteins. The present sequence represents a signal transduction	
CC	protein of the invention	
XX		
SQ	Sequence 374 AA;	
	Query Match 92.1%; Score 1798.5; DB 4; Length 374;	
	Best Local Similarity 90.8%; Pred. No. 6.9e-176;	
	Matches 335; Conservative 20; Mismatches 13; Indels 1; Gaps 1;	
QY	1 MDGAPVAEPRPTMTHGCRVLLYDIFGNKPEVTNKYOPPIPIGRGAYGIVCSVMNFETRE 60	
DB	6 VDGAPVAEPRQTTHGCRFLQYNIFGNLFETHKYQPPIMPGRGAYGIVCSVMNSETKE 65	
QY	61 MVAIKKIANAFNDMDAKTRLEIKLRLHLDHNIIGIRDVIPPPIPOAFNDVYIATELM 120	
DB	66 MVAIKKIANAFNDMDAKTRLEIKLRLHLDHNIIGIRDVIPPPIPOAFNDVYIATELM 125	
QY	121 DTDLHHIIRSNQELSEHCQFLYQLRGLKYTHSANVTHRDLKPSNLLNANCDLKICD 180	
DB	126 DTDLHHIIRSNQELSEHCQFLYQLRGLKYTHSANVTHRDLKPSNLLNANCDLKICD 185	
QY	181 FGLARPSSSDMMTEYVTVTRWRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLFPGR 239	
DB	186 FGLARPSSSDMMTEYVTVTRWRAPELLNSTDYSAAIDVWSVGCIFMELINRQPLFPGR 245	
QY	240 DHMHQRLITEVIGTDDDELGIARNEDAKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299	
DB	246 DHMHQRLITEVIGTDDDELGIARNEDAKYMRHLPOYPRRTFASMPFRVQPAALDLIE 305	
QY	300 RMLTFNPLQRTVBEALDHPYLERLHDIADBPICLEPFSEDFEQKALNEDQMKQLIFNEA 359	
DB	306 RMLTFNPLQRTVBEALDHPYLERLHDIADBPICLEPFSEDFEQKALNEDQMKQLIFNEA 365	
QY	360 IEMPNIRY 368	
DB	366 MELNPNRY 374	
XX		
XX	RESULT 4	
XX	AAG34158	
ID	AAG34158 standard; protein; 330 AA.	
XX		
AC	AAG34158;	
XX		
DT	18-OCT-2000 (first entry)	
XX		
DE	Zea mays protein fragment SEQ ID NO: 41519.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence; corn.	
XX		
OS	Zea mays subsp. mays.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999; 99US-0121825P.	
PR	05-MAR-1999; 99US-0123180P.	
PR	09-MAR-1999; 99US-0123548P.	
PR	23-MAR-1999; 99US-0125788P.	
PR	25-MAR-1999; 99US-0126264P.	
PR	29-MAR-1999; 99US-0126785P.	
PR	01-APR-1999; 99US-0127462P.	
PR	06-APR-1999; 99US-0128234P.	
PR	08-APR-1999; 99US-0128714P.	
PR	16-APR-1999; 99US-0129845P.	
PR	19-APR-1999; 99US-0130077P.	
PR	21-APR-1999; 99US-0130449P.	
PR	23-APR-1999; 99US-0130510P.	
PR	23-APR-1999; 99US-0130891P.	
PR	28-APR-1999; 99US-0131449P.	
PR	30-APR-1999; 99US-0132048P.	
PR	30-APR-1999; 99US-0132407P.	
PR	04-MAY-1999; 99US-0132484P.	
PR	05-MAY-1999; 99US-0132485P.	
PR	06-MAY-1999; 99US-0132486P.	
PR	06-MAY-1999; 99US-0132487P.	
PR	07-MAY-1999; 99US-0132863P.	
PR	11-MAY-1999; 99US-0134256P.	
PR	14-MAY-1999; 99US-0134218P.	
PR	14-MAY-1999; 99US-0134219P.	
PR	14-MAY-1999; 99US-0134221P.	
PR	14-MAY-1999; 99US-0134370P.	
PR	18-MAY-1999; 99US-0134768P.	
PR	19-MAY-1999; 99US-0134941P.	
PR	20-MAY-1999; 99US-0135124P.	
PR	21-MAY-1999; 99US-0135353P.	
PR	24-MAY-1999; 99US-0135629P.	
PR	25-MAY-1999; 99US-0136021P.	
PR	27-MAY-1999; 99US-0136392P.	
PR	28-MAY-1999; 99US-0136782P.	
PR	01-JUN-1999; 99US-0137222P.	
PR	03-JUN-1999; 99US-0137528P.	
PR	04-JUN-1999; 99US-0137502P.	
PR	07-JUN-1999; 99US-0137724P.	
PR	08-JUN-1999; 99US-0138094P.	
PR	10-JUN-1999; 99US-0138540P.	

Db	1	MPIGRGAYGIVCVNMNSETKEMVAIKKIANAFDNHMDAKRTLREIKLRLHLDHENIIGTR	60	PR	19-MAY-1999;	99US-0134941P.
Qy	100	DVIPPPIPOAFNDVIYATIELMDTDLHHIIRSNQELSEEHQCQFLYQILRGLKYIHSANVI	159	PR	20-MAY-1999;	99US-0135124P.
Db	61	DVIPPVPQAFNDVIYIGTELMDTDLHHIIRSNQELSEEHQYFLYQILRGLKYIHSANVI	120	PR	21-MAY-1999;	99US-0135353P.
Qy	160	HRDLKPSNLLLNANCDLKI CDFGLARPSSESMDMTYVTVRYRAPPELLNSTDYSA-D	218	PR	24-MAY-1999;	99US-0135629P.
Db	121	HRDLKPSNLLVNANCDLKI CDFGLARPSSESMDMTYVTVRYRAPPELLNSTDYSAAD	180	PR	25-MAY-1999;	99US-0136021P.
Qy	219	VNSVGCIFMELINRQPLFCGRDHMHQMRLLITEVIGTPTDDELGFIENEDARKYMRHLPOY	278	PR	27-MAY-1999;	99US-0136392P.
Db	181	VNSVGCIFMELINRQPLFCGRDHMHQMRLLITEVIGTPTDDELGFIENEDARKYMRHLPOF	240	PR	28-MAY-1999;	99US-0136782P.
Qy	279	PRRTFASMPFRVQPAALDIETRMFLTNPLQRTVVEBALDHPYLERLHDIADEPICLEPFS	338	PR	01-JUN-1999;	99US-0137222P.
Db	241	PRRPFVSLFRMPQPVALDIETRMFLTNPLQRTVVEBALDHPYLERLHDIADEPICLEPFS	300	PR	03-JUN-1999;	99US-0137528P.
Qy	339	FDFEQKALNEDQMKQILFNEAIEPMNPIRY	368	PR	04-JUN-1999;	99US-0137502P.
Db	301	FDFEQKALNEDQMKQILFNEAIEPMNPIRY	330	PR	07-JUN-1999;	99US-0137724P.
RESULT 5						99US-0138094P.
AAG34159						99US-0138540P.
ID AAG34159 standard; protein; 316 AA.						99US-0138847P.
XX	XX					99US-0139119P.
AC	AAG34159;					99US-0139452P.
XX	XX					99US-0139453P.
DT	18-OCT-2000 (first entry)					99US-0139492P.
XX	XX					99US-0139454P.
DE	Zea mays protein fragment SEQ ID NO: 41520.					99US-0139455P.
XX	XX					99US-0139456P.
KW	Protein identification; signal transduction pathway; metabolic pathway;					99US-0139457P.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;					99US-0139458P.
XX	termination sequence; corn.					99US-0139459P.
OS	Zea mays subsp. mays.					99US-0139750P.
XX	XX					99US-0139763P.
PN	EP1033405-A2.					99US-0139817P.
PD	06-SEP-2000.					99US-0139899P.
XX	XX					99US-0140353P.
PF	25-FEB-2000; 2000EP-00301439.					99US-0140354P.
XX	XX					99US-0140695P.
PR	25-FEB-1999;					99US-0140823P.
PR	05-MAR-1999;					99US-0140991P.
PR	09-MAR-1999;					99US-0141287P.
PR	23-MAR-1999;					99US-0141842P.
PR	29-MAR-1999;					99US-0142154P.
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PR	06-APR-1999;					99US-0142390P.
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PR	28-APR-1999;					99US-0144085P.
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PR	04-MAY-1999;					99US-0144331P.
PR	05-MAY-1999;					99US-0144332P.
PR	06-MAY-1999;					99US-0144333P.
PR	07-MAY-1999;					99US-0144334P.
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PR	18-MAY-1999;					99US-0145276P.
PR	18-MAY-1999;					99US-0145913P.
PR	18-MAY-1999;					99US-0145918P.
PR	18-MAY-1999;					99US-0145919P.

PR 28-JUL-1999; 99US-0145951P.
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 PR 25-AUG-1999; 99US-0150566P.
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 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
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 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
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 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.

PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.
 Query Match 79.7%; Score 1557.5; DB 3; Length 316;
 Best Local Similarity 92.7%; Pred. No. 3.5e-151;
 Matches 293; Conservative 12; Mismatches 10; Indels 1; Gaps 1;
 QY 54 MNFETREVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHENIIGIRDVIPPPIPOAFNDV 113
 DB 1 MNSETKEMVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHENIIGIRDVIPPVPQAFNDV 60
 QY 114 YIATELMDTDLHHIIRSNQELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLNAN 173
 DB 61 YIGTELMDTDLHHIIRSNQELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLNAN 120
 QY 174 CDLKICDFGLARPSSESMDMTEYVTRWRAPPELLINSTDYSAADVMSVGCIFMELINR 232
 DB 121 CDLKICDFGLARPSSESMDMTEYVTRWRAPPELLINSTDYSAADVMSVGCIFMELINR 180
 QY 233 QPLFGDRDHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOVPRRTFASMPFRVOP 292
 DB 181 QPLFGDRDHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOVPRRTFASMPFRVOP 240
 QY 293 AALDLIERMLTNPLQRTITVEBALDHPYLERLHDIADEPFCLEPFSFDFEQKALNEDQMK 352
 DB 241 VALDLIERMLTNPLQRTITVEBALDHPYLERLHDIADEPFCLEPFSFDFEQKALNEDQMK 300
 QY 353 QLIFNEAIEIEMNPRIY 368
 DB 301 QLIFNEAIEIEMNPRIY 316
 RESULT 6
 AAW15512
 ID AAW15512 standard; protein; 375 AA.
 XX
 AC AAW15512;
 XX
 DT 04-JUN-1997 (first entry)
 XX
 DE MAP kinase #1.
 KW Mitogen activated protein kinase; MAP; infectious specific protein;
 KW plant; jasnone acid.
 XX
 OS Synthetic.
 XX
 PN JP09065881-A.
 PD 11-MAR-1997.
 XX
 PF 29-AUG-1995; 95JP-00220935.
 XX
 PR 29-AUG-1995; 95JP-00220935.
 XX
 PA (NORQ) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
 XX
 DR WPI; 1997-220416/20.
 DR N-PSDB; AAT60349.
 XX
 PT Wound-stress inducible MAP kinase - used to regulate the synthesis of
 PT jasnone acid.
 PS Claim 2; Page 13-14; 21pp; Japanese.
 XX
 CC AAW15512 and AAW15513 represent the mitogen activated protein (MAP)
 CC kinases of the invention. This sequence contains the T-E-Y sequence, in
 CC which the threonine and tyrosine residues are phosphorylated to activate
 CC the protein at residues201-203. The MAP kinase and its gene can be used

CC to regulate the synthesis of jasmonone acid and the synthesis of a group of
 CC infectious specific proteins. By introducing the MAP kinase gene into a
 CC plant, thereby inducing expression of the mRNA for MAP kinase (or its
 CC antisense RNA), the synthesis of jasmonone acid and a group of infectious
 CC specific proteins can be regulated in the plant

XX SQ Sequence 375 AA;

Query Match 75.4%; Score 1472.5; DB 2; Length 375;
 Best Local Similarity 72.5%; Pred. No. 2.5e-142;
 Matches 263; Conservative 58; Mismatches 41; Indels 1; Gaps 1;
 QY 3 GAPVAEPRPTWTHGGRVLLYDIFGNKFEVTKYQPPIMPICRGAYGIVCSVMNPTREMV 62
 Db 10 GGOFPDPVPSVLTGGGVQVDFGNFPEITTKYRPPIMPICRGAYGIVCSVLNTELMW 69
 QY 63 AIKKIANAFNNDMDAKETLREIKLRLHDHENIIGIRDVTPPIPOAFNDVVIATELMDT 122
 Db 70 AVKKIANAFDIYMDAKETLREIKLRLHDHENIIGIRDVTPPIPOAFNDVVIATELMDT 129
 QY 123 DLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFG 182
 Db 130 DLHQIIRSNQGLSEHCQYFMYQLLRGLKYIHSANVLRDLKPSNLLVNAVNCOLKICDFG 189
 QY 183 LARPSSSDMMTEYVTVTRWTRAPPELLNSTDYSAADVWSVGCIFMELINRQPLFPGRDH 241
 Db 190 LARPNIENEMTEYVTVTRWTRAPPELLNSTDYTAADVWSVGCIFMELANRKPFGGKDH 249
 QY 242 MHQMRLLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQALDLIERM 301
 Db 250 VHQIRLLELIGTPTDDELGFQNEADAKRYIRQLPQHPROOLAEVFPVNPPLAIDLVDKM 309
 QY 302 LTFNPLQRIITVEALDHPYLERLHDIADEPICLEPFSDFEQKALNEDQMQLIFNEAIE 361
 Db 310 LTDPTRRIITVEALDHPYLAHLADAGDEPICVPFSPDEQQIGEEQIKDMYQEALS 369
 QY 362 MNP 364
 Db 370 LNP 372

RESULT 7
 AAB48048
 ID AAB48048 standard; protein; 398 AA.

XX AC AAB48048;
 XX DT 19-MAR-2001 (first entry)
 XX DE Signal transduction protein.
 XX Zm Zea mays; maize; signal transduction protein; phytohormone; ethylene;
 XX Kx auxin; cytokinin; gibberellin; immunogen.
 XX Os Zea mays.

XX W0200070059-A2.
 XX 23-NOV-2000.
 XX 28-APR-2000; 2000WO-US011687.
 XX 14-MAY-1999; 99US-0134292P.
 XX 08-JUL-1999; 99US-0142996P.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Helentjaris TG;
 XX WPI; 2001-031929/04.
 XX DR N-PSDB; AAC84265.
 XX New signal transduction nucleic acids and encoded proteins useful for

PT regulating phytohormone expression, including ethylene, auxins,
 PT cytokinins and gibberellin, to provide control of plant response to
 PT environmental stresses.

PS Claim 13; Page 97; 126pp; English.

XX The invention provides Zea mays signal transduction proteins and encoding
 CC nucleotide sequences. The nucleic acids are useful for regulating
 CC expression of phytohormones, including ethylene, auxins, cytokinins, and
 CC gibberellin, to effect developmental changes in plants and provide
 CC control of plant response to environmental stresses. They may also be
 CC used as probes or amplification primers in the detection, quantitation or
 CC isolation of gene transcripts, for detecting mutations in the gene, for
 CC monitoring upregulation of expression or changes in enzyme activity in
 CC screening assays of compounds, for detection of a number of allelic
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
 CC further be used for recombinant expression of their encoded polypeptides,
 CC as immunogens in the preparation or screening of antibodies, and in sense
 CC or antisense suppression of genes in a host cell, tissue or plant. The
 CC proteins may be used in assays for enzyme agonists or antagonists, as
 CC immunogens or antigens to obtain antibodies specifically immunoreactive
 CC with the proteins. The present sequence represents a signal transduction
 CC protein of the invention

XX SQ Sequence 398 AA;

Query Match 74.2%; Score 1448.5; DB 4; Length 398;
 Best Local Similarity 73.4%; Pred. No. 8.1e-140;
 Matches 268; Conservative 51; Mismatches 43; Indels 3; Gaps 3;
 QY 3 GAPVAE-PRPTWTHGGRVLLYDIFGNKFEVTKYQPPIMPICRGAYGIVCSVMNPTREMV 61
 Db 33 GAGMMENIATLSHGGRFIQYINFGNVFETSKYKPPILPIGKGYGIVCSALNSETARQ 92
 QY 62 VAIKKIANAFNNDMDAKETLREIKLRLHDHENIIGIRDVTPPIPOAFNDVVIATELMD 121
 Db 93 VAIKKIANAFNNDMDAKETLREIKLRLHDHENIIVAIRDIIPPPUREAFNDVVIATELMD 152
 QY 122 TDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 181
 Db 153 TDLHQIIRSNQALSEHCQYFLYQILRGLKYIHSANVLRDLKPSNLLNANCDLKICDF 212
 QY 182 GLARPSSSDMMTEYVTVTRWTRAPPELLNSTDYSAADVWSVGCIFMELINRQPLFPGRD 240
 Db 213 GLARTTSETDFMTYVTVTRWTRAPPELLNSTDYTAADVWSVGCIFMELMDRKLFPGRD 272
 QY 241 HMHQMRLLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQALDLIER 300
 Db 273 HVHQRLLELIGTPTNEADLDFV-NENARRYIRQLPCHAROSFPEKFPHVQPLAIDLVEK 331
 QY 301 MLTFNPLQRIITVEALDHPYLERLHDIADEPICLEPFSDFEQKALNEDQMQLIFNEAI 360
 Db 332 MLTFDPRQRIITVEGALAHFYLASLHDSDEPVCSPFSDFEQHALSEQMDLIYQEAL 391
 QY 361 EMNPN 365
 Db 392 AFNPD 396

RESULT 8
 AAG31654
 ID AAG31654 standard; protein; 382 AA.

XX AC AAG31654;
 XX DT 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 38049.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridization assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

OS	Arabidopsis thaliana.		
XX	EP1033405-A2.	PR	30-JUN-1999;
XX		PR	01-JUL-1999;
XX		PR	01-JUL-1999;
XX		PR	02-JUL-1999;
XX		PR	06-JUL-1999;
XX		PR	08-JUL-1999;
XX		PR	09-JUL-1999;
XX		PR	12-JUL-1999;
XX		PR	13-JUL-1999;
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XX		PR	27-JUL-1999;
XX		PR	28-JUL-1999;
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XX		PR	10-SEP-1999;
XX		PR	13-SEP-1999;
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		99US-0153758P.	

[illegible]

PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
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PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-014255P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
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PR 12-JUL-1999; 99US-0142877P.
PR 13-JUL-1999; 99US-0143842P.
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PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 07-SEP-1999; 99US-0152363P.
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PR 13-SEP-1999; 99US-0153758P.
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PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155133P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155565P.
PR 28-SEP-1999; 99US-0156450P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
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PR 12-OCT-1999; 99US-0158369P.
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PR 21-OCT-1999; 99US-0160741P.
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PR 25-OCT-1999; 99US-0161405P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 73.8%; Score 1442; DB 3; Length 395;

Best Local Similarity 72.4%; Pred. No. 3.7e-139;

Matches 270; Conservative 46; Mismatches 45; Indels 12; Gaps 3;

QY 3 GAPVAEFRP-----TWTHGGRYLLYDIFGNKFVTKYQPIPMPIGRGAYGIVCS 52

Db 20 GPPAAAPSPQMPGIENIPATLSHGGRFIQYINIFGNIFETAKYKPIPMPIGRGAYGIVCS 79

QY 53 VMNFETREVAIKKIANAFNNDMDAKRTLREIKLLRHLHDHENIIGIRDVIPPPIPOAFND 112

Db 80 AMNSETNESVAIKKIANAFDNKDARTLREIKLLRHMHDHENIVAIRDIIPPPLRNAFND 139

QY 113 VYIATELMDTLHRIIRSNOELSEBHCQYFLYQILRGLKYIHSANVHRDLKPSNLLNA 172

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Db      140 VYIAYELMTDLHQIIRSNQALSEEHCOFLYQILRGLKYIHSANVILHRDLKPSNLLNA 199
Qy      173 NCDLKICDFGLARPSSDMMTEYVYVTRVRAPELLNSTDYSAADVMSVGCIFMELIN 231
Db      200 NCDLKICDFGLARVTSESFMTEYVYVTRVRAPELLNSDITRAIDVMSVGCIFMELMD 259
Qy      232 ROPLFGRDHMHQMLRITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQ 291
Db      260 RKPLPGRDHWQRLLMELIGTSPSEELFLNENAKYIRQLPPYRQSIKDKPPTVH 318
Qy      292 PAALDIERMLTFNPLQRTVSEALDHPYLERLHDIADPEICLEPSPDFEQKALNEDQM 351
Db      319 PLAIDLIERKMLTFDPRRRTITVLDALAHPLYNSLHDSDEPCTIPNPFNFENHALSEEQM 378
Qy      352 KOLIFNEAJEMNP 364
Db      379 KELIYREALAFNP 391

RESULT 10
AAG31655
ID AAG31655 standard; protein; 366 AA.
XX
AC AAG31655;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38050.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123348P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
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XX 08-APR-1999; 99US-0128714P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
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PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
 Query Match 73.8%; Score 1441; DB 3; Length 366; Best Local Similarity 75.1%; Pred. No. 4.2e-119; Matches 266; Conservative 46; Mismatches 40; Indels 2; Gaps 2		
Qy	12	TMTGGRYLADYDFGNKPFVTKYQPIMPPIGRGAYGIVCSVMNPFETREMYAIKKIANAF 71 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	10	TLSHGGRFIQYNIFGNIFEVTAKYPKPIMPIGKYGAYGIVCSAMSETNESVAIKKIANAF 69 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy	72	NNDMDAKRTIREIKLLRLHDENIIGTRDVIPPPIPOAFNDVYIATELMDTDLHHIIIRSN 131 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	70	DNKIDAKRTIREIKLLRMDHENIVAIRDIPPFLRNAFNDVYIAYELMDTDLHQIIRSN 129 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy	132	QEISERHCOYFLVQLILGLKYHSANVIHRDLKPSNLLLNANCDLKICDGLARPSSESD 191 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	130	QALSEEHCOYFLVQLILGLKYHSANVIHRDLKPSNLLLNANCDLKICDGLARVTSSESD 189 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy	192	MMEYVVTVRWYRAPELLNSDYSA--DVMSVGCI FMELINRQPLFGGRDHMHQMRLITE 250 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	190	FMEYVVTVRWYRAPELLNSSDYTAADVMSVGCI FMELMDRKPLFGCRDVRHVQLRLWE 249 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy	251	VIGTPDDELGFTRNEDARKFMHLPOYPRRTFASMPRPVOPALDLLIERMLTFNPLORI 310 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	250	LIGTPSBEELFL--NENAKRYIRQLPPYPROSIDTKPPTVHPLAIDLIEKMILTFDPERRI 308 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy	311	TVREALDHPYLRLHDITADSPICLEPSDFEQKALNEDEOMKLI FNEAIEWNP 364 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	309	TVLDALAHPLYLNSLHDISDSPECTIPFNFDPENHALSEEQMKELIYREALAFNP 362 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
 RESULT 11 AAW61252 ID AAW61252 standard; protein; 393 AA. XX AC AAW61252; XX DT 22-SEP-1998 (first entry) XX DE Salicylic acid induced MAP kinase. XX KW Salicylic acid induced protein; SIP; mitogen-activated protein; MAP; KW tobacco; disease resistance; microbial pathogen; MAP kinase. XX OS Nicotiana sp. XX PN WO9818939-A1. XX PD 07-MAY-1998. XX PF 24-OCT-1997; 97WO-US019219. XX PR 25-OCT-1996; 96US-0029805P. PR 21-APR-1997; 97US-00837593. XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY. XX XK Klessig DF, Zhang S; PI WPI; 1998-272230/24. XX N-PsDB; AAV27563. XX FT Salicylic acid induced MAP kinase - obtained from tobacco, used to PT produce plants having increased disease resistance, against e.g. PT microbial pathogens. XX PS Claim 28; Page 62-63; 97pp; English. XX		
CC	This represents a salicylic acid induced protein (SIP) kinase. This SIP	
CC	kinase is an unique member of the mitogen-activated protein (MAP) kinase	
CC	family. The salicylic acid induced MAP kinase of the invention comprises	

KW Mitogen activated protein kinase; MAP; infectious specific protein;
 KW plant; jasmonate acid.
 XX Synthetic.
 OS
 XX JP09065881-A.
 PN
 XX 11-MAR-1997.
 PD
 XX
 XX 29-AUG-1995; 95JP-00220935.
 PF
 XX 29-AUG-1995; 95JP-00220935.
 PR
 XX (NORQ) NORINSUISANSHO NOGOYO SEIBUTSU SHIGEN.
 PA
 XX WPI; 1997-220416/20.
 DR
 XX N-PSDB; AAT60350.
 DR
 XX Wound-stress inducible MAP kinase - used to regulate the synthesis of
 PT jasmonate acid.
 PT
 XX
 XX Claim 3; Page 16-17; 21pp; Japanese.
 PS
 XX AAW15512 and AAW15513 represent the mitogen activated protein (MAP)
 CC kinases of the invention. This sequence contains the T-E-Y sequence, in
 CC which the threonine and tyrosine residues are phosphorylated to activate
 CC the protein at residues 249-251. The MAP kinase and its gene can be used
 CC to regulate the synthesis of jasmonate acid and the synthesis of a group of
 CC infectious specific proteins. By introducing the MAP kinase gene into a
 CC plant, thereby inducing expression of the mRNA for MAP kinase (or its
 CC antisense RNA), the synthesis of jasmonate acid and a group of infectious
 CC specific proteins can be regulated in the plant
 XX
 XX Sequence 423 AA;
 SQ
 Query Match 70.78; Score 1380.5; DB 2; Length 423;
 Best Local Similarity 72.38; Pred. No. 8.8e-133;
 Matches 253; Conservative 51; Mismatches 41; Indels 5; Gaps 3;
 QY 16 GGRYLLYDIFGNFVNTKQPTPIGRGAYGIVCSVMNFETREMAIKKIANAFNDM 75
 DB 75 GGRFA-AAAGNFPEITTKRPPIGRGAYGIVCSVLTNEMVAVKIANAFDIYM 133
 QY 76 DAKRTREIKLRLHLDHENIIGIRDVTPPIPOAFNDVYIATELMDTLHHIIRSNQELS 135
 DB 134 DAKRTREIKLRLHLDHENIIGIRDVTPPIPOAFNDVYIATELMDTLHHIIRSNQELS 190
 QY 136 EHCQVFLYQLRGLKVIHSANVTHRDLPKSNLLNANCDLKICDFGLARPSSSDMMTE 195
 DB 191 EDHCQVFLYQLRGLKVIHSANVTHRDLPKSNLLNANCDLKICDFGLARPSSSDMMTE 250
 QY 196 YVTRWTRAPPELLINSDYSA--DVMSVGCIFMELINRQPLFPGRDHQMLITEVIGT 254
 DB 251 YVTRWTRAPPELLINSDYSA--DVMSVGCIFMELINRQPLFPGRDHQMLITEVIGT 310
 QY 255 PTDELGFIRNEDARKYRHLPOYRTPFPASMPFRVQPAALDLIERMLTFNPQIRITVEE 314
 DB 311 PTEADLGLQNEADKRYIRLPQHPQBELAEVPHVNPFLAIDLVDKMLTFDPTRRITVEE 370
 QY 315 ALDHPYLERLHDINDEPICLEPSFDFEQALNEDQKQLIFNEAIEWNP 364
 DB 371 ALDHPYLERLHDINDEPICLEPSFDFEQALNEDQKQLIFNEAIEWNP 420
 RESULT 14
 ADX79753
 ID ADX79753 standard; protein; 318 AA.
 XX
 AC ADX79753;
 AC
 XX 21-APR-2005 (first entry)
 DT
 XX Plant full length insert polypeptide seqid 49119.
 DE

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX Unidentified.
 OS
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 XX 05-NOV-2001; 2001US-00985678.
 PR
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAK/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 XX Claim 1; SEQ ID NO 49119; 15pp; English.
 PS
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 XX Sequence 318 AA;
 SQ
 Query Match 68.6%; Score 1340.5; DB 8; Length 318;
 Best Local Similarity 77.1%; Pred. No. 7.7e-129;
 Matches 242; Conservative 46; Mismatches 25; Indels 1; Gaps 1;
 QY 52 SVMNFTREMAIKKIANAFNDMDAKRTREIKLRLHLDHENIIGIRDVIPPPIPOAFN 111
 DB 2 SLNLTETNELVAVKIANAFNDMDAKRTREIKLRLHLDHENIIGIRDVIPPPIPOAFN 61
 QY 112 DVYIATELMDTLHHIIRSNQELSEHCQVFLYQLRGLKVIHSANVTHRDLPKSNLLN 171
 DB 62 DVYIATELMDTLHHIIRSNQELSEHCQVFLYQLRGLKVIHSANVTHRDLPKSNLLN 121
 QY 172 ANCDLKICDFGLARPSSSDMMTEYVTRWTRAPPELLINSDY--SAADVWSVGCIFMELI 230

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2005, 04:38:30 ; Search time 4832 Seconds
(without alignments)

16422.487 Million cell updates/sec

Title: US-10-768-886-1
Perfect score: 1396
Sequence: 1 agagagtcagataaggtcgt.....ttaaaaaaaaaaaaaaaaaaaaaa 1396

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
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12: gb_un.*
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14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1396	100.0	1396	15	AF479883 Oryza sat
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ALIGNMENTS

RESULT 1

AF479883

LOCUS

DEFINITION Oryza sativa MAP kinase MAPK5a (MAPK5) mRNA, complete cds, alternatively spliced.

ACCESSION AF479883

VERSION AF479883.1

KEYWORDS GI:19401851

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 1396)

AUTHORS Xiong,L. and Yang,Y.

TITLE Disease Resistance and Abiotic Stress Tolerance in Rice Are Inversely Modulated by an Abscissic Acid-Inducible Mitogen-Activated Protein Kinase

JOURNAL Plant Cell 15 (3), 745-759 (2003)

PUBLISHED 12615946

REFERENCE 2 (bases 1 to 1396)

AUTHORS Xiong,L., Qi,M. and Yang,Y.

TITLE Molecular cloning and characterization of a novel MAP kinase, OSMAPK5, in rice

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1396)

AUTHORS Xiong,L., Qi,M. and Yang,Y.

TITLE Direct Submission

JOURNAL Submitted (01-FEB-2002) Plant Pathology, University of Arkansas, 217 Plant Science Building, Fayetteville, AR 72701, USA

FEATURES

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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 1396)
Xiong,L. and Yang,Y.
Disease Resistance and Abiotic Stress Tolerance in Rice Are
Inversely Modulated by an Abscissic Acid-Inducible Mitogen-Activated
Protein Kinase

Plant Cell 15 (3), 745-759 (2003)
12615946
Xiong,L., Qi,M. and Yang,Y.
Molecular cloning and characterization of a novel MAP kinase,
OSMAPK5, in rice

Unpublished
3 (bases 1 to 1396)
Xiong,L., Qi,M. and Yang,Y.
Direct Submission
Submitted (01-FEB-2002) Plant Pathology, University of Arkansas,
217 Plant Science Building, Fayetteville, AR 72701, USA

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VERSION AJ250311.1 GI:10862875
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SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1
AUTHORS Huang, H.-J., Dai, Y. H., Huang, D. D. and Kuo, T. T.
TITLE Molecular Cloning of a Low Temperature-Inducible MAP Kinase from
JOURNAL Rice
REFERENCE 2 (bases 1 to 1457)
AUTHORS Huang, H. J.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1999) Huang H. J., Department of Biology,
Cheng-Kung University, 1, University Rd., Tainan 701, TAIWAN
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ORIGIN

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Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Hara, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
12869764

REFERENCE AUTHORS

2 (bases 1 to 1411)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryū, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.

TITLE JOURNAL

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.
PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers
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FEATURES source

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Matches 1377; Conservative 0; Mismatch 1; Indels 0; Gaps 0;
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LOCUS AF332873
DEFINITION Oryza sativa MAP kinase BIMK1 mRNA, complete cds.
ACCESSION AF332873
VERSION AF332873.1 GI:12698875
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 1424)
Song, P. and Goodman, R.M.
OseBIMK1, a novel MAP kinase from rice that is involved in systemic
acquired resistance
Unpublished
REFERENCE
2 (bases 1 to 1424)
Song, P. and Goodman, R.M.
Direct Submission
JOURNAL
Submitted (30-DEC-2000) Department of Plant Pathology, University
of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 53706, USA
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Best Local Similarity 99.6%; Pred. No. 4.4e-182;
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RESULT 9
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LOCUS
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DEFINITION Triticum aestivum MAP kinase homolog (WCK-1) mRNA, complete cds.
ACCESSION AF079318
VERSION AF079318.1 GI:3396051
KEYWORDS .
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE 1 (bases 1 to 1452)
AUTHORS Takezawa, D.
TITLE Rictor- and A23187-induced expression of WCK-1, a gene encoding
mitogen-activated protein kinase in wheat
JOURNAL Plant Mol. Biol. 40 (6), 921-933 (1999)
PUBMED 10527417
REFERENCE 2 (bases 1 to 1452)
AUTHORS Takezawa, D.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1998) Basic Cryoscience, Institute of Low
Temperature Science, Hokkaido University, Kita 19 Nishi 8, Sapporo
060, Japan
FEATURES
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Triticum aestivum MAP kinase homolog (WCK-1) mRNA, complete cds.
AF079318
AF079318.1 GI:3396051
Triticum aestivum (bread wheat)
Triticum aestivum
1 (bases 1 to 1452)
Takezawa, D.
Rictor- and A23187-induced expression of WCK-1, a gene encoding
mitogen-activated protein kinase in wheat
Plant Mol. Biol. 40 (6), 921-933 (1999)
10527417
2 (bases 1 to 1452)
Takezawa, D.
Direct Submission
Submitted (21-JUL-1998) Basic Cryoscience, Institute of Low
Temperature Science, Hokkaido University, Kita 19 Nishi 8, Sapporo
060, Japan

Location/Qualifiers
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 VERSION X79993.1 GI:871983
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 SOURCE Avena sativa (oat)
 ORGANISM Avena sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Aveneae; Avena.
 1
 Huttly,A.K. and Phillips,A.L.
 Gibberellin-regulated expression in oat aleurone cells of two
 kinases that show homology to MAP kinase and a ribosomal protein
 kinase
 JOURNAL Plant Mol. Biol. 27 (5), 1043-1052 (1995)
 PUBMED 7766874

REFERENCE

2 (bases 1 to 1520)
 Huttly,A.K.
 Direct Submission
 Submitted (30-JUN-1994) A.K. Huttly, Institute of Arable Crops
 Research, Univ. of Bristol, Dept of Agricultural Sciences, Long
 Ashton Research Station, Bristol, BS18 9AF, UK

FEATURES

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RESULT 12
AF479884 1084 bp mRNA linear PLN 04-MAR-2003
LOCUS
DEFINITION
Oriza sativa MAP kinase MAPK5b (MAPK5) mRNA, complete cds,
alternatively spliced.

ACCESSION
AF479884
VERSION
AF479884.1 GI:19401853

KEYWORDS
SOURCE
ORGANISM
Oriza sativa
Oriza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
Xiong,L. and Yang,Y.
Disease Resistance and Abiotic Stress Tolerance in Rice Are
Inversely Modulated by an Abscisic Acid-Inducible Mitogen-Activated
Protein Kinase

JOURNAL
PUBMED
12615946
REFERENCE
2 (bases 1 to 1084)

AUTHORS
TITLE
Xiong,L., Qi,M. and Yang,Y.
Molecular cloning and characterization of a novel MAP kinase,
OsMAPK5, in rice

JOURNAL
REFERENCE
3 (bases 1 to 1084)

AUTHORS
TITLE
Xiong,L., Qi,M. and Yang,Y.
Direct Submission

JOURNAL
SUBMITTED (01-FEB-2002) Plant Pathology, University of Arkansas,
217 Plant Science Building, Fayetteville, AR 72701, USA

FEATURES
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ORIGIN
Query Match 57.9%; Score 808.4; DB 15; Length 1084;

Best Local Similarity 99.9%; Pred. No. 3.9e-103;
Matches 809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 587 GAAACGCAACTCGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCCGCTGTCGAGAG 646
Db 275 GATCGCAACTCGGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCCGCTGTCGAGAG 334

Qy 647 CGACATGATGACGAGTAGTGTGTCAACCGGTGTACCGCGCGCGGAGCTGTCTCAA 706
Db 335 CGACATGATGACGAGTAGTGTGTCAACCGGTGTACCGCGCGCGGAGCTGTCTCAA 394

Qy 707 CTCACCGCACTACTCCGCGCCATCGACGTCTGGTCCGTGGTGTCTTTCATGAGCT 766
Db 395 CTCACCGCACTACTCCGCGCCATCGACGTCTGGTCCGTGGTGTCTTTCATGAGCT 454

Qy 767 CATCAACCGCCAGCGCTCTTCCCGGCGAGGACCAATGACAGATGCGCTCATCAC 826
Db 455 CATCAACCGCCAGCGCTCTTCCCGGCGAGGACCAATGACAGATGCGCTCATCAC 514

Qy 827 CGAGGTGATCGGAGCGCCCGACGACGACGAGCTGGGTTTCATACGGAACGAGACGCGAG 886
Db 515 CGAGGTGATCGGAGCGCCCGACGACGACGAGCTGGGTTTCATACGGAACGAGACGCGAG 574

Qy 887 GAAGTACATGAGGACCTCGCCGACGACGACGACGACGACGACGACGACGACGACGACG 946
Db 575 GAAGTACATGAGGACCTCGCCGACGACGACGACGACGACGACGACGACGACGACGACG 634

Qy 947 GGTGAGCCCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAG 1006
Db 635 GGTGAGCCCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAG 694

Qy 1007 AATCAGATGTAGGAGCGCTCGATCATCTTACCTAGAGAGATTGACGACATCGCCGA 1066
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Qy 1127 CCAATGAAGCAGCTGATCTTCAACGAGCGATCGAGATGAACCCAAACATCCGGTACTA 1186
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Qy 1367 GAACTTTGGATTAATAAAAAAAAAAAAAAAAAAAAAA 1396
Db 1055 GAACTTTGGATTAATAAAAAAAAAAAAAAAAAAAAAA 1084

RESULT 13
AB016801
LOCUS
DEFINITION
Zea mays mRNA for MAP kinase 4, complete cds.

ACCESSION
AB016801
VERSION
AB016801.1 GI:4239886
KEYWORDS
MAP kinase 4; ZmMPK4.

SOURCE
Zea mays
ORGANISM
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (sites)

AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Berberich, T., Sano, H. and Kusano, T.
 Involvement of a MAP kinase, ZmMPK5, in senescence and recovery
 from low-temperature stress in maize
 Mol. Gen. Genet. 262 (3), 534-542 (1999)
 10589842
 2 (bases 1 to 1647)
 Kusano, T.
 Direct Submission
 Submitted (07-AUG-1998) Tomonobu Kusano, Nara Institute of Science
 and Technology, Research and Education Center for Genetic
 Information; 8916-5 Takayama-cho, Ikoma, Nara 630-0101, Japan
 (E-mail: kusano@bs.ais-t-nara.ac.jp, Tel: 81-743-72-5651,
 Fax: 81-743-72-5659)

FEATURES

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ORIGIN

Query Match 57.4%; Score 800.8; DB 15; Length 1647;
 Best Local Similarity 81.8%; Pred. No. 4.2e-102; Indels 90; Gaps 1;
 Matches 977; Conservative 0; Mismatches 127;

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 DB 230 TCTTCGGGAACAAGTTCGAGGTGACGAGCAAGTACGAGCGCTCCCGTCATGCCCATCGGCC 289
 QY 208 GCGGCGCTACGGGATCGTCTGCTCGTATGAACTTTGAGACGAGGAGATGGTGGCA 267
 DB 290 GCGGCGCTACGGGATCGTCTGCTCGTATGAACTTTGAGACGAGGAGATGGTGGCA 349
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 DB 350 TCAAGAGATCGCCACGCGTTTCGACCAACCAATGACGCGCGGCGGCGGAGCA 409
 QY 328 TCAAGTCTCTAGGACCTCGACACGAGAAATCATATAGGATCAGGAGATGATCCGCG 387
 DB 410 TCAAGTCTTAAGGACCTCGACACGAGAAATCATATAGGATCAGGAGATGATCCGCG 469
 QY 388 CGCGGATCCCTCAGGCGTTCAACGAGCTCTACATCGCCACGAGCTCATGGACACGACC 447
 DB 470 CGCGGCTCCGCGAGGTTCAACGAGCTCTACATCGGACGAGCTGATGGACACGACC 529
 QY 448 TCCATCATCATCTCCGCTCCACACGAGAACTGTGAGAGACGACATGCCAGTATTTCTGT 507
 DB 530 TGCACCATCATCTCCGCTCCACACGAGAGCTCTCGGAGGACATCCCACTGATCTCTGT 589
 QY 508 ACCAGATCTCGCGGGGCTCAGTATCATCATCGCGGAACTGATCCACCGCGACCTGA 567

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 QY 568 AGCCGAGCAACCTGCTGCTGAAACGCAACTCGACCTCAAGATCTGCGACTTCGGGCTGG 627
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 QY 808 ACCAGATCGCTCATCACCG-----AGGTGATCG 837
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 QY 898 GGCACTCTCCGAGTACCCGCGCGGAGCTTTCGGGAGCATGTTCCCGGGTGCAGCCCG 957
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 QY 1078 GCCTGGAGCCCTTCTTCGACTTCGAGCAGAGGCTTCTAAACGAGGACCAATGAAGC 1137
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 QY 1138 AGCTGATCTTCAACGAGCGGATCGAGATGACCAACCAACATCGGTACTAGATTG 1191
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RESULT 14
 AY642433
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AY642433
 Brassica napus cultivar Huyou15 mRNA linear PLN 06-JUL-2005
 mRNA, complete cds.
 AY642433.1 GI:54402039
 Brassica napus (rape)
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 (bases 1 to 1464)
 Yu, S., Zhang, L., Zuo, K., Tang, D. and Tang, K.
 Isolation and characterization of an oilseed rape MAP kinase BnMPK3
 involved in diverse environmental stresses
 Plant Sci. 169 (2), 413-421 (2005)
 2 (bases 1 to 1464)
 Yu, S., Zhang, L., Zuo, K., Tang, D. and Tang, K.
 Direct Submission
 Submitted (01-JUN-2004) Agriculture and Biology, Plant

Biotechnology Research Center, 1954# Huashan Road, Shanghai 200030,
China

FEATURES

Source

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ORIGIN

Query Match 41.4%; Score 577.6; DB 15; Length 1464;
Best Local Similarity 69.7%; Pred. No. 5.2e-71;
Matches 781; Conservative 0; Mismatches 339; Indels 0; Gaps 0;
QY 54 AGAAGAGAGGAGGAGGATTAGGATCGACGGCGCGGTGGCGGAGTTTCAGCGCAGC 113
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QY 114 ATGACGACGCGCGCGGTCTCTCTACGACATCTTCGGGAAACAAAGTTTCGAGGTGACG 173
DB 196 CAGAGCGACGAGGACAGTTTCATAAGCTACGATATCTTCGGTAGTTTATTCGAGGTCA 255
QY 174 AACAGTACAGCGCGCCCATCATGCCATTGGCGCGCGCGCTACGGGATCGTCTGCTCC 233
DB 256 TCCAAGTACCGTCTCCGATTGTTTCCAACTCGTGGCGGCATACGGCATCGTTTGTCT 315
QY 234 GTGATGAATTTAGAGAGGAGATGCTGCGCATAAAGATCGCCAAAGCGTTTCAAC 293
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QY 294 AACGACATGACGACGACGACGCTCGGGAGATCAAGCTCTCTCAGGACCTCGACAC 353
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QY 414 GTCTACATCGCCGAGGATCATGGACACGACCTCCATCATCATCCGCTCCAAACCA 473
DB 496 GTTTATATCGCCATCGAGTTAATGGACATGATCTTATCAATCAATCATCATCAACCA 555
QY 474 GAACTGTGAGAGACGCTGCGAGTATTTCTGTACCATGATCTCTCGCGGGCTCAAGTAC 533
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QY 534 ATCCATCTCGGGAAACGTTGATCCACCGGACCTGAAAGCGGAGCAACCTGCTGTGAAGCC 593
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QY 594 AACTGCGACCTCAGATCTCGACTTCGGCTTCGGCTGCGCGCGCTGCTCGGAGGCGCATG 653
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QY 654 ATGACGAGATGACGTGTCACCGGTGTTACCGCGCGCGGAGCTGCTGCTCAATCCAC 713
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DB 916 CTTGGCACGCGCAGACAGATCAGATCTCGGGTTTACACAAACGAGGATGCCAAAAGATAC 975
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DB 976 ATCCGCGAGTTCCCAACTTCCTCCGCCAACCGTTAGCTTAACTGTTCTCTCATGTTAA 1035
QY 954 CCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAGAAATCACA 1013
DB 1036 TCATTGGCCATTGATCTAGTTGACAGAAATGTTGACGCTTTGACCCCAACGAAGATCACT 1095
QY 1014 GTTGAGAGCGCTCGATCATCTTACCTTAGAGAGATTGACGACATCGCGGATGAGCCC 1073
DB 1096 GTTGAAGAAAGCTCTGAATCACCGGTACCTAGCCAAAGTTGACGACCGCAATGATGAGCCA 1155
QY 1074 ATCTGCTCGAGCGCTTCTCTTCTCGACTTCGAGCAGAGGCTCTAAACGAGGACCAATG 1133
DB 1156 ATCTGCTAAGCCATCTCTTCTCGACTTTGAAACAACAACCTCTAGACGAGGACAGATA 1215
QY 1134 AACGAGCTGATCTTCAACGAAGCGATCGAGATGAACCCAA 1173
DB 1216 AAGAGATGATCTACAGGAGGACCATTCCTCAATCCAA 1255

RESULT 15

AY805424

LOCUS

Chorisporea bungeana 1419 bp mRNA linear PLN 28-NOV-2004
complete cds.

ACCESSION

AY805424

VERSION

AY805424.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

ORIGIN

Query Match

Score

DB

Length

1419;

Best Local Similarity 68.4%; Pred. No. 2.2e-68;
Matches 773; Conservative 0; Mismatches 357; Indels 0; Gaps 0;

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Db	76	ATAGAGAGAGAAAGATGNACCGCGGCGCCAGTTTCACAGATTTCCCGCGGTGCAAC	135
Qy	119	GCACGGCGCGGTACTGCTCTACGACATCTTTGGGAACAAGTTTCGAGGTGACGACAA	178
Db	136	TCAATGGAGGACAGTTTCATAAGTTACGATATCTTCGGTAGTCTATTCGAGATCACATCAA	195
Qy	179	GTACCAAGCCGCCCATCATGCCCATTTGGCGCGCGCTACGGGATCGTCTGCTCCGTGAT	238
Db	196	GTATCGCCCTCCGATCATACCAATCGCGCGCGCATATGGAATCGTATGCTCCGTGTT	255
Qy	239	GAACTTTGAGACGAGGAGATGTTGGCATTAAGAAGATCGCCAACGCGTTCAACAACGA	298
Db	256	GGATTGGGAGACGACGAGCTGGTGGGATGAAGAAGTAGCGNACGCCCTTCGATANTCA	315
Qy	299	CATGAGCGCAAGCGCACGCTCCGGGAGATCAAGCTCTCAGGCACCTCGACCAAGAA	358
Db	316	CATGAGCGCAAGCGTACACTTCGCGAGATCAAGCTCCTTGGCCATCTAGATCATGAAA	375
Qy	359	CATCATAGGATCAGGGATGTGATCCGCGCGCGATCCCTCAGGCGTTCAACGAGCTTA	418
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Qy	419	CATCGCACGGAGCTCATGGACACCGACCTCCATCACATCATCCGCTCCAACCAAGAACT	478
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Qy	479	GTGAGAGAGACTGCGCAGTATTTCTGTACAGATCTTCGCGGGGCTCAAGTACATCCA	538
Db	496	GTGAGAGGACACTGTCACTACTTCTGTACAGCTTCTTCGAGGGCTCAAGTACATCCA	555
Qy	539	CTCGCGNAGCTGATCCACCGGACCTGAAGCGGACCACTCTCTGTAACGCCAACTG	598
Db	556	CTCGGCTAAGCTTATTACAGGGATTTAAAGCCCAAGCAATCTTCTCTGAACGCAATTG	615
Qy	599	CGACCTCAAGATCTGGACTTCGGGCTGGCGGCGTCTGCGGAGCGCATGATGAC	658
Db	616	CGATTTAAGATCTGCGATTTTCGGTCTTGTAGACCACTTCAGAGAACGATTTATGAC	675
Qy	659	GGAGTACGTGGTCAACCGGTGTTACCGCGCGCGGAGCTCTGCTCAACTCCAACGACTA	718
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Qy	719	CTCGCGGCCATCGAGTCTGGTCCGTGCGCTGCATCTTCATGAGCTCATCAACGCCA	778
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Qy	779	GCGGCTCTTCCCGGAGGACCAACATGACACGATGCGCCTCATCCGAGGTGATCGG	838
Db	796	GCTTTTGTTCCTCCGGTAAGACCAGTGTCCATCAATGCGTTTATTGACAGAGTTGCTTG	855
Qy	839	GACGCCGACGACGAGCTGGGGTTTCATA CGGAACGAGGACGCGAGGAAGTACATGAG	898
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Qy	899	GCACCTGCGCAGTACCGCGCGCGGAGGTTTCGGGAGCATGTTCCCGGGGTGAGCCCG	958
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Qy	1019	GGAGGCGCTGATCATCTTCTACCTAGAGAGATTGACGACATCGCGGATGAGCCCATCTG	1078
Db	1036	AGAAGCTCTGNAACCAACCACTGACCTAGCCAAATTCGACGACCCCAATGATGAGCCCATCTG	1095
Qy	1079	CTGGGAGCCCTTCTCTCGACTTCGAGCGAAGGCTCTTAACGAGGACCAATGAGCA	1138

Db	1096	TCAAAAGCCATTCTCTTTTGAGTTGGAACAACAGCCTATGGACGTGGAAACAGATAAAGA	1155
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Search completed: December 29, 2005, 06:38:08
Job time : 4838 secs